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Sire by environment interactions for growth traits in beef cattle

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SIRE BY ENVIRONMENT INTERACTIONS FOR GROWTH TRAITS IN BEEF CATTLE

Iowa State University PH.D. 1983

Sire by environment interactions for growth traits in beef cattle

by

Joseph Keith Bertrand

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INTRODUCTION

Several beef breed associations have recently introduced national sire evaluation programs. With the widespread use of artificial insemination, development of mixed model evaluation techniques and the availability of performance data provided by breeders, it is possible to evaluate beef sires for their expected progeny performance over a wide range of environmental and management conditions. A major problem that must be addressed is the nature and importance of sire by environment interactions in field data sire evaluation. Some sire by environmental interactions can be controlled by a structured progeny testing program; others cannot be controlled but need to be considered as part of the evaluation procedure.

The objective of this study was to determine the nature and magnitude of sire by environment interactions in beef cattle field data. Birth weight, weaning weight and postweaning gain were investigated to determine the importance of region by sire, herd within region by sire, and contemporary group within herd by sire interactions in the prediction of future progeny performance.

REVIEW OF LITERATURE

Environment by Sire Interactions

Dickerson (1962) lists environmental factors which can modify the expression or evaluation of a given genetic difference and thus produce sire by environment or genotype by environment interactions. Some of these environmental factors are:

1) External physical influences: temperature, humidity, feeding regimes, pathogens, etc.;
2) Maternal effects: A dam's environmental influence on her offspring is partly due to her own genotype and partly due to her environment;
3) Effects of gene interaction and internal influences: These consist of epistatic effects, dominance deviation, sex limited traits, and other internal influences that control the expression of genotype;
4) Social Environment: An example would be the effect of social dominance on percentage of calves sired by natural service sires in multi-sire cow groups.

In beef cattle field data, it cannot be assumed that cows were randomly bred to sires and all progeny were given equal treatment within a contemporary group; therefore, significant estimates of contemporary group by sire or herd by sire interactions may be due to an extra correlation among paternal offspring besides genetic causes through the sire. Bereskin and Lush (1965) explained that this extra correlation was due to correlated environmental effects, correlations between breeding values of the mates of the sires, correlations

between the breeding values of the sire and his mates, and correlations involving both environmental and genetic effects. This extra correlation between progeny of the same sire would be a direct result of nonrandom mating and preferential treatment of cows and/or progeny. Wilson (1983) observed evidence of nonrandom mating in Angus breeding herds. Dams that were artificially serviced had significantly higher estimated breeding value ratios for weaning weight than naturally serviced dams. Also, more popular AI sires were not usually mated to the younger females but rather to older females. Zollinger and Nielson (1983) found evidence in 15 Angus herds of positive assortative mating practices. They observed that all the herds in the study tended to mate higher merit dams to bulls of higher genetic merit. Schaeffer et al. (1978) reported positive correlations between dam weaning weight expected transmitting abilities and sire weaning weight expected progeny differences. The correlations ranged from .26 to .35 for the Angus, Charolais, Hereford and Shorthorn breeds.

The structure of field data suggests several interactions which could have an impact on future sire evaluations. A hierarchal division of environmental effects into regions, herds within region and contemporary groups within herd can be accomplished. These three environmental effects may be composed of sex, years, seasons, feeding regimes, management practices and other physical environmental factors. Several studies, using beef cattle growth traits, have examined the interaction of genotype of sire with several types of environmental effects.

Pahnish et al. (1961), Tanner et al. (1970) and Thrift et al. (1970)

found little evidence of sex by sire interactions for weaning weight or postweaning gain. Bradley et al. (1966) reported no significant sex by sire interactions for birth weight; however, Buchanan and Nielson (1979) found evidence of significant sex by sire interactions for birth weight and weaning weight.

In studies examining ration by sire interaction, Ahlschwede et al. (1969) and Dillard et al. (1964) found no significant interaction effects for weaning weight and postweaning gain. In a study using identical twin Holstein heifers, Ramsey and Freeman (1965) reported no significant ration by genotype interaction for body weights measured at three-month intervals.

Reports on the importance of year by sire and season by sire interactions are varied. Kennedy and Henderson (1975) found substantial year by sire interactions for weaning weights of Hereford and Angus purebred calves; however, no evidence of year by sire interaction was reported for postweaning gain. In studies using Hereford calves, Pahnish et al. (1961) reported no significant year by sire interaction for weaning weight, and Pani et al. (1973) found significant year by sire interaction for postweaning gain. Brown and Gacula (1962) reported no significant year-season by sire interaction for weaning weight. In a study using Maine-Anjou Association field data, Buchanan and Nielson (1979) reported a significant season by sire effect for weaning weight.

In studies using American Simmental Association field data, Burfening et al. (1982) found a herd within region by sire variance equal to the sire variance, and Tess et al. (1979) found a similar result for birth weight.

Buchanan and Nielson (1979), using American Simmental Association and Maine-Anjou Association field data, found significant herd within region by sire interactions for weaning weight but not for birth weight. Ahlschwede et al. (1969) and Brown and Gacula (1962) found no evidence of herd within region by sire interactions for postweaning gain.

Wilson et al. (1972) examined herd by sire interactions for birth weight, weaning weight and postweaning gain. The data came from herds located in South Dakota, Montana, Wyoming and Alberta, Canada. There was no evidence of any significant herd by sire interactions for the three traits.

Nunn et al. (1978) found significant region of the United States by sire interaction for weaning weight but not for birth weight. The genetic correlation between sire weaning weight expected progeny differences (EPDs) in different regions was calculated as .73. Robertson (1959) reported that a genetic correlation of .8 or lower suggests that rank changes between genotypes are occurring in different environments.

Using field data and mixed models that included region by sire and herd within region by sire random effects, Burfening et al. (1982) found no significant region by sire interaction for birth weight; however, Buchanan and Nielson (1979) found that region by sire interactions were important sources of variation for both traits. Buchanan and Nielson (1979) found that the genetic correlation between sire EPDs in different regions for the two traits ranged from .30 to .80. Tess et al. (1979) found that region by sire interactions were not significant for weaning weight; however, the region by sire variance was nearly half the size of the sire variance.

In general, it appeared that location (either herds within regions, regions, or both) by sire interactions were sufficiently large to cause biases in sire breeding value estimation.

Heritability

Table 1 contains a summary of literature heritability estimates for birth weight, weaning weight and postweaning gain reported by Woldehawariat et al. (1977). Most studies included in the summarization estimated heritability on a within-herd basis.

Table 2 contains a summary of across regions and across herds within region heritability estimates for birth weight, weaning weight and post-weaning gain.

The estimates of across region and across herds within region heritabilities reported in the literature for the three traits were usually less than the estimates summarized in Table 1. If region by sire or herd within region by sire interactions exist, heritability estimates across regions and across herds within regions should be less than within herd heritability estimates.

Table 1. Summary of heritability estimates for birthweight, weaning weight and postweaning gain reported by Woldehawariat et al. (1977)

Trait	Method	Weighted	Number of Estimates	h^2
Birth weight	Overall	No	84	.39
	Parent-offspring reg.	No	7	.38
	Parent-offspring reg.	Yes	7	.42
	Paternal half sib (PHS)	No	68	.40
	Paternal half sib (PHS)	Yes	68	.40
	Weighted reg. and weighted PHS	Yes	75	.45
Weaning weight	Overall	No	103	.31
	Parent-offspring reg.	No	11	.31
	Parent-offspring reg.	Yes	11	.13
	Paternal half sib (PHS)	No	72	.32
	Paternal Half sib (PHS)	Yes	72	.26
	Weighted reg. and weighted PHS	Yes	83	.24
Postweaning gain	Overall	No	44	.45
	Parent-offspring reg.	No	7	.53
	Parent-offspring reg.	Yes	7	.47
	Paternal half sib (PHS)	No	36	.44
	Paternal half sib (PHS)	Yes	36	.32
	Weighted reg. and weighted PHS	Yes	43	.34

Table 2. Summary of across region and across herd within region heritability estimates for birth weight, weaning weight and postweaning gain

Trait	Author and date	Across region h^2 estimate	Across herd within region h^2 estimate	Data source
Birth weight	Buchanan and Nielson (1979)	.06	.11	Simmental field data
	Burfening et al. (1982)	.18	.18	Simmental field data
	Massey and Benyshek (1981)	.16		Limousin field data
	Nunn et al. (1978)	.22		Simmental field data
	Wilson et al. (1972)	.26		Angus herds from S. Dakota, Wyoming, Montana and Alberta
	"	.15		Hereford herds from S. Dakota, Wyoming, Montana and Alberta
	Overall average	.17	.15	
Weaning weight	Buchanan and Nielson (1979)	.21	.27	Maine-Anjou field data
	"	.07	.24	Simmental field data
	Massey and Benyshek (1981)	.10		Limousin field data
	Nunn et al. (1978)	.06		Simmental field data
	Tess et al. (1979)	.06	.09	Simmental field data
	Wilson et al. (1972)	.22		Angus herds from S. Dakota, Wyoming, Montana and Alberta
	"	.25		Hereford herds from S. Dakota, Wyoming, Montana and Alberta
	Overall average	.14	.20	
Postweaning gain	Massey and Benyshek (1981)	.08		Limousin field data
	Wilson et al. (1972)	.45		Angus herds from S. Dakota, Wyoming, Montana and Alberta
	"	.26		Hereford herds from S. Dakota, Wyoming, Montana and Alberta
	Overall average	.26		

MATERIALS AND METHODS

Data Description

Three growth traits from registered Polled Hereford calves were provided for statistical analyses by the American Polled Hereford Association (APHA). The data were all birth weight, weaning weight and postweaning gain records from January 1964 to July 1981.

The weaning weight records, adjusted for age of dam and to 205 days of age, were from 247,943 calves. The birth weight records, adjusted for age of dam and sex of calf, were from 68,271 calves. The postweaning gain records were created by finding the difference between 365-day, 452-day or 550-day adjusted yearling weight and 205-day adjusted weaning weight. The postweaning gain records were composed of 160-day, 247-day or 345-day adjusted postweaning gain.

The data used in this study were from the data set used to generate the APHA 1982 Sire Summary. The APHA 1982 Sire Summary was a report listing the expected future progeny performance of the breed's extensively used sires. Approximately 98% of the data was collected by cattlemen participating in the APHA Guide Lines Program. The remaining 2% was collected by APHA staff from the Gold Seal Program. The Gold Seal Program was a designed progeny testing program comparing breeder owned bulls with designated reference sires.

The objective of this study was to determine the effect of region by sire, herd within region by sire and contemporary group within herd by sire interactions on mixed model national sire evaluation.

The contemporary group definition for birth weight was herd code,

weaning date and sex group. For weaning weight, herd code, weaning date, sex group and weaning management code (creep or no creep) defined a contemporary group. The contemporary group definition for postweaning gain was herd code, yearling weigh date, sex group, weaning management code and yearling management code (365-, 452-, or 550-day adjusted).

The United States was divided into nine regions using procedures presented by Leighton (1979). Each region was defined by taking into consideration average levels of rainfall, temperature, forage production, management practices and terrain characteristics. Zip codes were used to define geographic regions free from state line boundaries. The nine regions were labeled as Northeast, Cornbelt, South, Gulf Coast, Upper Plains, Lower Plains, Rocky Mountains, Desert Southwest and Pacific. Figure 1 presents the nine regions as defined in this study.

To estimate the effect of herd within region by sire and contemporary group within herd by sire interactions, the data were first separated by region. Table 3 contains the number of records in each region. The data in each of the nine regions were edited to include only those records from pairs of sires with progeny together in at least two herds within the region and in at least two contemporary groups within each herd. Each sire was also required to have at least two or more progeny in half of the contemporary groups within a herd. Table 3 contains the number of sires, herds, contemporary groups within herd, herd by sire cells, contemporary group within herd by sire cells and total progeny left in each region after the records were edited for each trait.

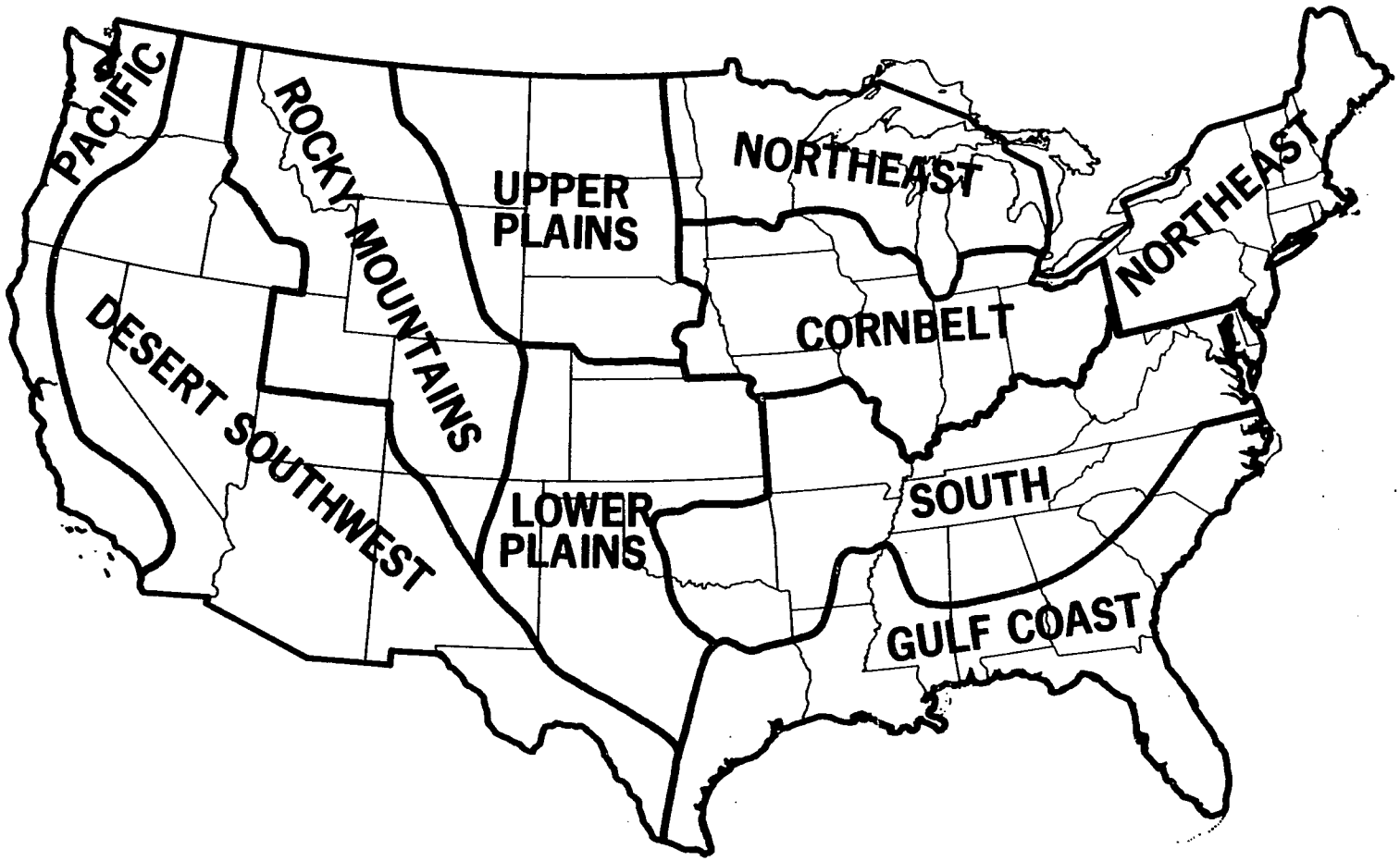

Figure 1. Boundary definitions for nine geographic regions of the United States.

Table 3. Description of data for the estimation of variance components for birth weight, weaning weight and postweaning gain in each region of the United States

Region	Total records[a]	Final records[b]	Herds	Contemporary groups	Sires	Herd by sire cells	C. group by sire cells
				Birth Weight			
Northeast	9217	1076	23	165	30	82	402
Cornbelt	12355	2332	32	144	95	249	674
South	10467	216	8	37	10	20	87
Gulf Coast	3670	238	6	21	6	16	54
Upper Plains	6859	421	10	39	18	36	105
Lower Plains	9358	132	8	27	8	18	57
Rocky Mts.	5818	37	2	7	2	4	14
Desert S.W.	3998	136	4	14	4	8	28
Pacific	6529	167	5	29	8	16	60
				Weaning Weight			
Northeast	23938	2416	50	384	60	191	951
Cornbelt	35273	4233	56	309	133	364	1141
South	39624	1287	30	170	40	105	423
Gulf Coast	16308	1032	20	125	32	85	334
Upper Plains	40110	4967	51	413	122	291	1288
Lower Plains	51420	2786	51	345	84	184	902
Rocky Mts.	15808	1172	13	135	30	72	389
Desert S.W.	11546	409	8	51	13	27	124
Pacific	13916	1201	16	129	32	73	318

				Postweaning gain			
Northeast	11156	869	16	120	25	65	319
Cornbelt	13949	2028	19	99	79	196	541
South	12564	368	10	34	12	30	99
Gulf Coast	4574	181	5	23	9	20	65
Upper Plains	18374	970	16	67	23	51	169
Lower Plains	17463	539	11	49	21	42	140
Rocky Mts.	7201	446	8	43	12	27	108
Desert S.W.	5223	59	2	7	2	4	14
Pacific	8286	982	10	78	24	53	199

[a]Number of records in each region before data were edited.

[b]The final records, herds, C. groups, sires, herd by sire cells and C. group by sire cells were the number of observations or cells available after the data in each group were edited to estimate sire by environment effects.

Editing the data in this manner reduced the data set to a manageable size without losing any herd by sire and contemporary group within herd by sire cells that would contribute to the estimation of herd by sire and contemporary group within herd by sire and error variance components.

To estimate the effect of region by sire interactions, the original data set was edited to include only those records from pairs of sires with progeny in at least two regions. The sire pairs were also required to have progeny together in at least one herd in one of the regions and in two herds in the other region and progeny together in at least two contemporary groups within each herd. Again, the sires were required to have at least two or more progeny in half of the contemporary groups in each herd. The restriction that each sire pair have progeny in at least two herds within each region was relaxed to obtain more region by sire cells. Table 4 presents the number of regions, herds within region, contemporary groups within herd, sires, region by sire, herd within region by sire cells, contemporary group within herd by sire cells and total progeny available for each trait after the editing process to create region by sire cells.

Models

Two models were used in this analysis. One was a within-region model, and the other an across-region model. The same models were used for each trait.

Table 4. Description of data for the estimation of variance components birth weight, weaning weight and postweaning gain across regions of the United States

	Birth weight	Weaning weight	Postweaning gain
Total records[a]	68271	247943	98790
Final records[b]	2263	8569	1800
Regions	6	9	9
Herds	39	181	38
C. groups	224	1123	160
Sires	33	92	36
Region by sire cells	86	313	84
Herd by sire cells	154	664	140
C. groups by sire cells	624	2957	430

[a]Number of records before data was edited.

[b]The final records, regions, herds, C. groups, sires, region by sire cells, herd by sire cells, C. group by sire cells was the number of observations or cells available after the data was edited to estimate sire by environment effects.

The within-region model was:

$$Y_{jklm} = \mu + H_j + Cg_{jk} + S_l + HS_{jl} + CgS_{jkl} + e_{jklm} \quad (1)$$

Y_{jklm} = the observation of the m^{th} calf of the l^{th} sire in the k^{th} contemporary group in the j^{th} herd,

μ = overall mean within region,

H_j = the fixed effect of the j^{th} herd,

Cg_{jk} = the fixed effect of the k^{th} contemporary group in the j^{th} herd,

S_l = the random effect of the l^{th} sire,

HS_{jl} = the random effect of the interaction between the j^{th} herd and the l^{th} sire

CgS_{jkl} = the random effect of the interaction between the k^{th} contemporary group in the j^{th} herd and the l^{th} sire.

e_{jklm} = random error.

Basic assumptions were:

$E[Y] = XB_{FE}$ where B_{FE} represents the fixed effects of model (1).

$E[S_l] = E[HS_{jl}] = E[CgS_{jkl}] = E[ejklm] = 0.$

$$\text{Var}\begin{bmatrix} S \\ HS \\ CgS \\ e \end{bmatrix} = \begin{bmatrix} I\sigma^2_{S(1)} & 0 & 0 & 0 \\ & I\sigma^2_{HS} & 0 & 0 \\ & & I\sigma^2_{CgS} & 0 \\ & & & I\sigma^2_{e(1)} \end{bmatrix}$$

The across-region model was:

$$Y_{ijklm} = \mu + R_i + H_{ij} + Cg_{ijk} + S_l + RS_{il} + HS_{ijl} + CgS_{ijkl} + e_{ijklm} \quad (2)$$

Y_{ijklm} = the observation of the m^{th} calf of the l^{th} sire in the k^{th} contemporary group in the j^{th} herd in the i^{th} region,

μ = overall mean across regions,

R_i = the fixed effect of the i^{th} region,

H_{ij} = the fixed effect of the j^{th} herd in the i^{th} region,

Cg_{ijk} = the fixed effect of the k^{th} contemporary group in the j^{th} herd in the i^{th} region,

S_l = the random effect of the l^{th} sire,

RS_{il} = the random effect of the interaction between the i^{th} region and the l^{th} sire,

HS_{ijl} = the random effect of the interaction between the j^{th} herd in the i^{th} region and the l^{th} sire,

CgS_{ijkl} = the random effect of the interaction between the k^{th} contemporary group in the j^{th} herd in the i^{th} region and the l^{th} sire.

e_{ijklm} = random error.

The assumptions for the across-region model were:

$E[Y] = XB_{FE}$ where B_{FE} represents the fixed effects of model (2).

$E[S_l] = E[RS_{il}] = E[HS_{ijl}] = E[CgS_{ijkl}] = E[e_{ijklm}] = 0$.

$$\text{Var}\begin{bmatrix} S \\ RS \\ HS \\ CgS \\ e \end{bmatrix} = \begin{bmatrix} I\sigma^2_{S(2)} & 0 & 0 & 0 & 0 \\ & I\sigma^2_{RS} & 0 & 0 & 0 \\ & & I\sigma^2_{HS} & 0 & 0 \\ & & & I\sigma^2_{CgS} & 0 \\ & & & & I\sigma^2_{e(2)} \end{bmatrix}$$

Variance component estimates for model (1) and model (2) random effects were estimated using Henderson (1953) Method 3 techniques.

The strategy of this procedure was to choose reductions in sums of squares, which are quadradic forms, find their expectations under the full model and use linear combinations of these quadradic forms to yield variance component estimates unaffected by fixed effects.

Statistical and Computational Procedures

Some matrix and statistical properties and definitions that were useful in the performance of Henderson Method 3 variance estimation procedures can be found in Searle (1971). Some of these theories and definitions were:

1. $(X'X)^-$ is a generalized inverse of $X'X$ if $X'X(X'X)^-X'X = X'X$.
2. If $(X'X)^-$ is a generalized inverse of $X'X$, then $X(X'X)^-X'X = X$ and $X'X(X'X)^-X' = X'$.

3. A matrix is idempotent if the product with itself is equal to itself. $X(X'X)^{-}X'$ and $[I-X(X'X)^{-}X']$ are idempotent matrices.
4. The trace (tr) of a matrix is equal to the sum of the diagonal elements of that matrix.
5. The trace of matrix products is cyclically commutative $\therefore tr(ABC) = tr(CAB) = tr(BCA)$.
6. The rank of an idempotent matrix is equal to its trace.
7. The rank of X = rank $X'X$ = rank of $X(X'X)^{-}X'$.
8. If $Y = XB + e$ where B represents fixed and random effects and $cov(B,e) = 0$ and $E[ee'] = I\sigma_e^2$, then $E(YY') = E[(XB+e)(XB+e)']$ $= XE[BB']X' + I\sigma_e^2$.
9. Let $Y'QY$ be a quadradic form, then

$$E(Y'QY) = E[tr(Y'QY)] = tr[QE(YY')]$$
$$= tr(QXE[BB']X') + trQ\sigma_e^2$$
$$= tr(X'QXE[BB']) + \sigma_e^2 \text{ tr } Q.$$

To compute the variance components for sire, herd by sire, contemporary group within herd by sire and error from model (1), six reductions or quadradic forms were used. These reductions were:

$$R(\mu \text{ H Cg S HS CgS}) = Y'X(X'X)^{-}X'Y = \sum_{jkl} Y_{jkl.}^2/N_{jkl.}$$

X = the incidence matrix for all the effects from model (1).

$R(\mu\ H\ Cg) = Y'X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}Y = \sum_{jk} Y^2_{jk..}/N_{jk..}$

X_{FE} = the incidence matrix for the fixed effects for model (1).

$R(\mu\ H\ S\ HS) = Y'X_2(X'_2X_2)^{-}X'_2Y = \sum_{j1} Y^2_{j.1.}/N_{j.1.}$

X_2 = the incidence matrix for herd, sire and herd by sire effects from model (1).

$R(\mu\ H\ Cg\ S) = R(\mu\ H\ Cg) + R(S/\mu\ H\ Cg)$

$R(S/\mu\ H\ Cg) = Y'Q_iY = \tilde{S}'X'_SS_iY$

where $\tilde{S} = (X'_SS_iX_S)^{-}X'S_iY$,

$S_i = I-X'_{FE}(X'_{FE}X_{FE})^{-}X_{FE}$,

$Q_i = S_iX_S(X'_SS_iX_S)^{-}X'_SS_i$,

X_S = incidence matrix for sire effects from model (1).

$R(\mu\ H\ Cg\ S\ HS) = R(\mu\ H\ S\ HS) + R(Cg/\mu\ H\ S\ HS)$

$R(Cg/\mu\ H\ S\ HS) = Y'Q_jY = \tilde{Cg}'X'_{cg}S_jY$

where $\tilde{Cg} = (X'_{cg}S_jX_{cg})^{-}X'S_jY$

$S_j = [I-X_2(X'_2X_2)^{-}X'_2]$

$Q_j = S_jX_{cg}(X'_{cg}S_jX_{cg})^{-}X'_{cg}S_j$

X_{Cg} = the incidence matrix for the contemporary group effects from model (1).

$$Y'Y = \sum_{jklm} Y^2_{jklm}.$$

The expectations of these reductions are:

$$E[R(\mu\ H\ Cg\ S\ HS\ CgS)] = E[Y'X(X'X)^{-}X'Y],$$

$$= \text{tr}\ E[B'X'X(X'X)^{-}X'XB] + \sigma^2_{e_{(1)}}\ \text{tr}[X(X'X)^{-}X'],$$

$$= \text{tr}\ (X'XE[BB']) + \sigma^2_{e_{(1)}}\ \text{rank}\ (X'X),$$ where B = the vector of solutions for the fixed and random effects from model (1),

$$= \text{tr}\begin{bmatrix} X'_{FE}X_{FE}E[B_{FE}B'_{FE}] & X'_{FE}X_S I\sigma^2_{S_{(1)}} & X'_{FE}X_{HS} I\sigma^2_{HS} & X'_{FE}X_{CgS} I\sigma^2_{CgS} \\ & X'_S X_S I\sigma^2_{S_{(1)}} & X'_S X_S\ I\sigma^2_{HS} & X'_S X_{CgS}\ I\sigma^2_{CgS} \\ & & X'_{HS}X_{HS}I\sigma^2_{HS} & X'_{HS}X_{CgS}\ I\sigma^2_{CgS} \\ & & & X'_{CgS}X_{CgS}I\sigma^2_{Cgs} \end{bmatrix}$$

$$+ \sigma^2_{e_{(1)}}\ \text{rank}\ (X'X).$$

X_{HS} = incidence matrix for herd by sire effects from model (1),

X_{CgS} = incidence matrix for contemporary group within herd by sire effects from model (1),

B_{FE}, B_S, B_{HS} and B_{CgS} = the vector of solutions from model (1) corresponding to the subscripts.

$$E[R(\mu\ H\ Cg)] = E[Y'X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}Y],$$

$$= \text{tr}\ E[B'X'X_{FE}\ (X'_{FE}X_{FE})^{-}X'_{FE}X\ B] + \sigma e^2_{(1)}\text{tr}[X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}],$$

$$= \text{tr}(X'X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}\ X\ E[B'B]) + \sigma e^2_{(1)}\ \text{rank}\ (X'_{FE}X_{FE}).$$

Let $H_{FE} = X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}$, then the above reduction is

$$= \text{tr}\begin{bmatrix} X'_{FE}X_{FE}E[B_{FE}B'_{FE}] & X'_{FE}X_S\ I\sigma^2_{S_{(1)}} & X'_{FE}X_{HS}\ I\sigma^2_{HS} & X'_{FE}X_{CgS}\ I\sigma^2_{CgS} \\ & X'_S H_{FE}X_S I\sigma^2_{S_{(1)}} & X'_S H_{FE}X_{HS}\ I\sigma^2_{HS} & X'_S H_{FE}X_{CgS} I\sigma^2_{CgS} \\ & & X'_{HS}H_{FE}X_{HS}I\sigma^2_{HS} & X'_{HS}H_{FE}X_{CgS}\ I\sigma^2_{CgS} \\ & & & X'_{CgS}H_{FE}X_{CgS}I\sigma^2_{CgS} \end{bmatrix}$$

$$+ \sigma^2_{e_{(1)}}\ \text{rank}\ (X'_{FE}X_{FE}).$$

$$E[R(\mu\ H\ S\ HS)] = E[Y'X_2(X'_2X_2)^{-}X'_2Y],$$

$$= \text{tr}\ E[B'X'X_2(X'_2X_2)^{-}X'_2XB] + \sigma e^2_{(1)}\ \text{tr}(X_2(X'_2X_2)^{-}X'_2),$$

$$= \text{tr}(X'X_2(X'_2X_2)^{-}X'_2\ X\ E[BB']) + \sigma e^2_{(1)}\ \text{rank}\ (X'_2X_2),$$

let $H_2 = [X_2(X'_2X_2)^{-}X'_2]$, then

$$= \operatorname{tr}\begin{bmatrix} X_H'X_{FE}E[B_{FE}B_H'] & X_H'X_{FE}E[B_{FE}B_{Cg}'] & X_H'X_S I\sigma^2_{S(1)} & X_H'X_{HS} I\sigma^2_{HS} & X_H'X_{CgS} I\sigma^2_{CgS} \\ & X_{Cg}'H_2X_{FE}E[B_{FE}B_{Cg}'] & X_{Cg}'X_S I\sigma^2_{S(1)} & X_{Cg}'X_{HS} I\sigma^2_{HS} & X_{Cg}'H_2X_{CgS} I\sigma^2_{CgS} \\ & & X_S'X_S I\sigma^2_{S(1)} & X_S'X_{HS} I\sigma^2_{HS} & X_S'X_{CgS} I\sigma^2_{CgS} \\ & & & X_{HS}'X_{HS} I\sigma^2_{HS} & X_{HS}'X_{CgS} I\sigma^2_{CgS} \\ & & & & X_{CgS}'H_2X_{CgS} I\sigma^2_{CgS} \end{bmatrix}$$

$$+ \sigma^2_{e(1)} \text{ rank } (X_2'X_2).$$

$$E[R(S/\mu \ H \ Cg)] = E[Y'Q_iY],$$

$$= \text{tr } E[B'X'Q_i \ X \ B] + \sigma^2_{e(1)} \text{ tr } Q_i,$$

$$= \text{tr } (X'Q_i \ X \ E[BB']) + \sigma^2_{e(1)} \text{ rank } (X_S'S_iX_S),$$

$$= \operatorname{tr}\begin{bmatrix} 0 & 0 & 0 & 0 \\ & X_S'S_iX_S I\sigma^2_{S(1)} & X_S'S_iX_{HS} I\sigma^2_{HS} & X_S'S_iX_{CgS} I\sigma^2_{CgS} \\ & & X_{HS}'Q_iX_{HS} I\sigma^2_{HS} & X_{HS}'Q_iX_{CgS} I\sigma^2_{CgS} \\ & & & X_{CgS}'Q_iX_{CgS} I\sigma^2_{CgS} \end{bmatrix}$$

$$+ \sigma^2_{e(1)} \text{ rank } (X_S'S_iX_S).$$

$$E[R(Cg/\mu\ H\ S\ HS)] = E[Y'Q_jY],$$

$$= \text{tr}\ E[B'X'Q_j\ X\ B] + \sigma_{e(1)}^2\ \text{tr}\ Q_j,$$

$$= \text{tr}\ (X'Q_j\ X\ E[BB']) + \sigma_{e(1)}^2\ \text{rank}\ (X'_{Cg}S_jX_{Cg}),$$

$$= \text{tr}\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ & X'_{Cg}S_jX_{FE}\ E[B_{FE}B'_{Cg}] & 0 & 0 & X'_{Cg}S_jX_{CgS}\ I\sigma^2_{CgS} \\ & & 0 & 0 & 0 \\ & & & 0 & 0 \\ & & & & X'_{CgS}S_jX_{CgS}\ I\sigma^2_{CgS} \end{bmatrix}$$

$$+ \sigma_e^2 \text{rank}\ (X'_{Cg}S_jX_{Cg})$$

$$E[Y'Y] = \text{tr}\ E[B'X'X\ B + I\sigma_e^2],$$

$$= \text{tr}\ (X'X\ E[BB']) + N\sigma_e^2$$

where N = number of total progeny available for model (1) analysis.

By choosing appropriate linear combinations of reductions, it is possible to get unbiased variance component estimates.

$$E[R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ Cg)]$$

$$= k_1\sigma^2_{S(1)} + k_2\sigma^2_{HS} + k_3\sigma^2_{CgS} + k_4\sigma^2_{e(1)}.$$

Where $k_1 = tr\ (X_S' S_i X_S)$,

$k_2 = tr\ (X_{HS}' S_i X_{HS})$,

$k_3 = tr\ (X_{CgS}' S_i X_{CgS})$,

$k_4 = rank\ (X'X) - rank\ (X_{FE}' X_{FE})$.

$$E[R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ Cg\ S\ HS)]$$

$$= E[R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ Cg) - R(S/\mu\ H\ Cg)],$$

$$= k_5\ \sigma^2_{HS} + k_6\sigma^2_{CgS} + k_7\sigma^2_{e(1)}.$$

Where $k_5 = tr\ (X_{HS}' S_i X_{HS}) - tr\ (X_{HS}' Q_i X_{HS})$,

$k_6 = tr\ (X_{CgS}' S_i X_{CgS}) - tr\ (X_{CgS}' Q_i X_{CgS})$,

$k_7 = rank\ (X'X) - rank\ (X_{FE}' X_{FE}) - rank\ (X_S' S_i X_S)$.

$$E[R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ Cg\ S\ HS)]$$

$$= [R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ S\ HS) - R(Cg/\mu\ H\ S\ HS)],$$

$$= k_8\sigma^2_{CgS} + k_9\sigma^2_{e(1)}.$$

Where $k_8 = tr\ (X_{CgS}' S_j X_{CgS}) - tr\ (X_{CgS}' Q_j X_{CgS})$,

$k_9 = rank\ (X'X) - rank\ (X_2' X_2) - rank\ (X_{Cg}' S_j X_{Cg})$.

$$E[Y'Y - R(\mu\ H\ Cg\ S\ HS\ CgS)]$$

$$= k_{10}\sigma^2_{e(1)}$$

Where $k_{10} = N - rank\ (X'X)$.

Table 5 contains the values for the k-coefficients for the variance components from model (1) for birth weight, weaning weight and postweaning gain for each region of the United States. Using these four linear combinations of reductions, it was possible to get estimates for $\sigma^2_{S(1)}$, σ^2_{HS}, σ^2_{CgS} and $\sigma^2_{e(1)}$.

To compute the variance components for sire, region by sire and error from model (2), four additional reductions were used. The variance components for σ^2_{HS} and σ^2_{CgS} from the nine within-region analyses were pooled together by weighting each region's variance component estimates by the degrees of freedom available for the herd by sire or contemporary group within herd by sire random effect. The weighted estimates of σ^2_{HS} and σ^2_{CgS} were used in the model (2) variance component estimation equations, since the expectations of σ^2_{HS} and σ^2_{CgS} were the same for model (1) and model (2). The expected value of $\sigma^2_{S(1)}$ was not the same as $\sigma^2_{S(2)}$ because of the hierarchal structure of regions, herds within regions and contemporary groups within herds. The expected value of $\sigma^2_{e(1)}$ was not the same as $\sigma^2_{e(2)}$ due to the different editing procedures between the within-region analyses and the across-region analyses for obtaining herds within regions.

The reductions used to estimate the variance components from model (2) were:

$$R(\mu\ R\ H\ Cg\ S\ RS\ HS\ CgS) = Y'X(X'X)^{-}X'Y = \sum_{ijkl} Y^2_{ijkl.}/N_{ijkl.}.$$

X = incidence matrix for all the effects for model (2).

Table 5. The k-coefficients for the variance components from the within region models for birth weight, weaning weight and postweaning gain for each region of the United States

Region	k_1[a]	k_2	k_3	k_4	k_5[b]	k_6	k_7	k_8[c]	k_9	k_{10}[d]
					Birth Weight					
Northeast	511.6	511.6	511.6	137	196.4	445.8	114	380.9	181	674
Cornbelt	1713.7	1713.7	1713.7	530	859.7	1327.9	438	907.1	315	559
South	103.3	103.3	103.3	50	43.2	87.6	44	74.9	38	129
Gulf Coast	110.1	110.1	110.1	33	29.8	84.4	28	72.3	23	184
Upper Plains	245.8	245.8	245.8	66	70.9	175.1	53	141.2	40	316
Lower Plains	59.6	59.6	59.6	30	19.2	47.2	25	39.3	20	75
Rocky Mts.	13.5	13.5	13.5	7	6.0	11.3	6	9.4	5	23
Desert S.W.	42.3	42.3	42.3	14	15.6	34.3	12	27.3	10	108
Pacific	72.3	72.3	72.3	31	24.8	54.3	26	44.4	22	107
					Weaning Weight					
Northeast	1182.9	1182.9	1182.9	567	544.7	1040.1	514	875.0	431	1465
Cornbelt	2706.8	2706.8	2706.8	832	1354.4	2179.3	708	1588.8	528	3092
South	654.5	654.5	654.5	253	241.7	539.1	220	458.6	185	864
Gulf Coast	520.6	520.6	520.6	209	228.4	433.2	183	354.3	153	698
Upper Plains	3032.0	3032.0	3032.0	875	903.1	2560.1	770	2242.3	646	3679
Lower Plains	1495.1	1495.1	1495.1	557	441.7	1270.7	494	1124.8	431	1884
Rocky Mts.	644.9	644.9	644.9	254	266.6	560.8	230	471.6	198	783
Desert S.W.	179.4	179.4	179.4	73	83.8	152.1	64	124.4	55	285
Pacific	620.1	620.1	620.1	189	255.5	483.9	163	383.6	137	883

				Postweaning Gain						
Northeast	444.2	444.2	444.2	199	177.5	375.4	177	310.6	151	550
Cornbelt	1496.0	1496.0	1496.0	442	708.1	1161.8	365	831.7	268	1487
South	239.1	239.1	239.1	65	73.0	190.2	55	162.7	45	269
Gulf Coast	90.8	90.8	90.8	42	40.2	68.3	34	51.1	27	116
Upper Plains	546.6	546.6	546.6	102	150.1	439.8	85	388.1	68	801
Lower Plains	309.3	309.3	309.3	91	81.2	229.5	75	194.1	26	399
Rocky Mts.	217.6	217.6	217.6	65	83.4	176.3	56	145.3	46	338
Desert S.W.	14.2	14.2	14.2	7	5.7	11.8	6	9.7	5	45
Pacific	507.1	507.1	507.1	121	181.5	372.6	102	293.3	82	783

[a] $R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ Cg) = k_1\sigma^2_{S_{(1)}} + k_2\sigma^2_{HS} + k_3\sigma^2_{CgS} + k_4\sigma^2_{e_{(1)}}$.

[b] $R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ Cg\ S) = k_5\sigma^2_{HS} + k_6\sigma^2_{CgS} + k_7\sigma^2_{e_{(1)}}$.

[c] $R(\mu\ H\ Cg\ S\ HS\ CgS) - R(\mu\ H\ Cg\ S\ HS) = k_8\sigma^2_{CgS} + k_9\sigma^2_{e_{(1)}}$.

[d] $Y'Y - R(\mu\ H\ Cg\ S\ HS\ CgS) = k_{10}\sigma^2_{e_{(1)}}$.

$$R(\mu\ R\ H\ Cg) = Y'X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}Y = \sum_{ijk} Y^2_{ijk../N_{ijk..}} \qquad (10)$$

X_{FE} = incidence matrix for the fixed effects for model (2).

$$R(\mu\ R\ H\ Cg\ S) = R(\mu\ R\ H\ Cg) + R(S/\mu\ R\ H\ Cg)$$

$$R(S/\mu\ R\ H\ Cg) = Y'Q_kY = \tilde{S}'X'_SS_kY$$

where $\tilde{S} = (X'_SS_kX_S)^{-}\ X'_SS_kY$

$$S_k = I - [X_{FE}(X'_{FE}X_{FE})^{-}\ X'_{FE}],$$

$$Q_k = S_kX_S(X'_SS_kX_S)^{-}\ X'_SS_k,$$

X_S = incidence matrix for sire effects from model (2).

$$Y'Y = \sum_{ijklm} Y^2_{ijklm}$$

The expectations of these reductions are:

$$E[R(\mu\ R\ H\ Cg\ S\ RS\ HS\ CgS)] = E[Y'X(X'X)^{-}\ X'Y],$$

$$= \text{tr}\ E[B'X'X(X'X)^{-}\ X'XB] + \sigma^2_{e(2)}\ \text{tr}\ [X(X'X)^{-}\ X'],$$

$$= \text{tr}\ (X'X\ E[BB']) + \sigma^2_{e(2)}\ \text{rank}\ (X'X),$$ where B = the vector of solutions for the fixed and random effects from model (2).

$$= \begin{bmatrix} X'_{FE}X_{FE}[\bar{\sigma}_{FE}B'_{FE}]^{1} & & & & \\ & X'_{FE}X_S\, I\sigma^2_{S(2)} & X'_{FE}X_{RS}\, I\sigma^2_{RS} & X'_{FE}X_{HS}\, I\sigma^2_{HS} & X'_{FE}X_{CgS}\, I\sigma^2_{CgS} \\ \text{tr} & X'_SX_S I\sigma^2_{S(2)} & X'_SX_{RS}\, I\sigma^2_{RS} & X'_SX_{HS}\, I\sigma^2_{HS} & X'_SX_{CgS}\, I\sigma^2_{CgS} \\ & & X'_{RS}X_{RS} I\sigma^2_{RS} & X'_{RS}X_{HS}\, I\sigma^2_{HS} & X'_{RS}X_{CgS}\, I\sigma^2_{CgS} \\ & & & X'_{HS}X_{HS} I\sigma^2_{HS} & X_{HS}X_{CgS}\, I\sigma^2_{CgS} \\ & & & & X'_{CgS}X_{CgS} I\sigma^2_{CgS} \end{bmatrix}$$

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[1] This is the diagonal element of the fixed effects row.

$+ \sigma^2_{e(2)}$ rank (X'X).

X_{RS} = incidence matrix for region by sire effects from model (2),

X_{HS} = incidence matrix for herd within region by sire effects from model (2),

X_{CgS} = incidence matrix for contemporary group within herd by sire effects from model (2),

B_{FE}, B_S, B_{RS}, B_{HS} and B_{CgS} = the vector of solutions from model (2) corresponding to the subscripts.

$$E[R(\mu\ R\ H\ Cg)] = Y'X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}Y,$$

$$= \text{tr } E[B'X'X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}XB] + \sigma^2_{e(2)} \text{ tr}[X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}],$$

$$= \text{tr } (X'X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}X\ E[B'B]) + \sigma^2_{e(2)} \text{ rank } (X'_{FE}X_{FE})$$

let $H_{FE} = X_{FE}(X'_{FE}X_{FE})^{-}X'_{FE}$, then

$$= \begin{bmatrix} X'_{FE}X_{FE}[B_{FE}B'_{FE}]^{1} & & & & \\ X'_{FE}X_S\, I\sigma^2_{S(2)} & X'_{FE}X_{RS}\, I\sigma^2_{RS} & X'_{FE}X_{HS}\, I\sigma^2_{HS} & X'_{FE}X_{CgS}\, I\sigma^2_{CgS} & \\ X'_S H_{FE} X_S I\sigma^2_{S(2)} & X'_S H_{FE} X_{RS}\, I\sigma^2_{RS} & X'_S H_{FE} X_{HS}\, I\sigma^2_{HS} & X'_S H_{FE} X_{CgS}\, I\sigma^2_{CgS} & \\ & X'_{RS} H_{FE} X_{RS} I\sigma^2_{RS} & X'_{RS} H_{FE} X_{HS}\, I\sigma^2_{HS} & X'_{RS} H_{FE} X_{CgS}\, I\sigma^2_{CgS} & \\ & & X'_{HS} H_{FE} X_{HS} I\sigma^2_{HS} & X'_{HS} H_{FE} X_{CgS}\, I\sigma^2_{CgS} & \\ & & & X'_{CgS} H_{FE} X_{CgS} I\sigma^2_{CgS} & \end{bmatrix}$$

$$+ \sigma^2_{e(2)} \text{ rank } (X'_{FE}X_{FE}).$$

$$E[R(S/\mu\ R\ H\ Cg)] = E[Y'Q_kY],$$

$$= \text{tr } E[B'X'Q_kXB] + \sigma^2_{e(2)} \text{ tr } Q_k,$$

$$= \text{tr } (X'Q_kX\ E[BB']) + \sigma^2_{e(2)} \text{ rank } X'_S S_k X_S,$$

---

[1] This is the diagonal element of the fixed effects row.

$$= \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ & X_S'S_kX_S I\sigma^2_{S(2)} & X_S'S_kX_{RS} I\sigma^2_{RS} & X_S'X_kX_{HS} I\sigma^2_{HS} & X_S'S_kX_{CgS} I\sigma^2_{CgS} \\ & & X_{RS}'Q_kX_{RS} I\sigma^2_{RS} & X_{RS}'Q_kX_{HS} I\sigma^2_{HS} & X_{RS}'Q_kX_{CgS} I\sigma^2_{CgS} \\ & & & X_{HS}'Q_kX_{HS} I\sigma^2_{HS} & X_{HS}'Q_kX_{CgS} I\sigma^2_{CgS} \\ & & & & X_{CgS}'Q_kX_{CgS} I\sigma^2_{CgS} \end{bmatrix}$$

$$\text{tr} + \sigma^2_{e(2)} \text{ rank } (X_S'S_kX_S).$$

$$E[Y'Y] = \text{tr } E[B'X'XB + I\sigma_e^2],$$

$$= \text{tr } (X'X \; E[BB']) + N\sigma_e^2$$

where N = number of total progeny available for model (2) analysis.

Again, by choosing appropriate linear combinations of reductions, it is possible to get unbiased variance component estimates.

$$E[R(\mu \; R \; H \; Cg \; S \; RS \; HS \; CgS) - R(\mu \; R \; H \; Cg)]$$

$$= K_{11}\sigma^2_{S(2)} + K_{12}\sigma^2_{RS} + K_{13}\sigma^{2*}_{HS} + K_{14}\sigma^{2*}_{CgS} + K_{15}\sigma^2_{e(2)}.$$

Where $K_{11} = \text{tr } (X_S'S_kX_S)$,

$K_{12} = \text{tr } (X_{RS}'S_kX_{RS})$,

$K_{13} = \text{tr } (X_{HS}'S_kX_{HS})$,

$K_{14} = \text{tr } (X_{CgS}'S_kX_{CgS})$,

$K_{15} = \text{rank } (X'X) - \text{rank } (X_{FE}'X_{FE})$,

σ^{2*}_{HS} = weighted average estimate of herd within region by sire variance component from model (1),

σ^{2*}_{CgS} = weighted average estimate of contemporary group within herd by sire variance component from model (1).

$$E[R(\mu\ R\ H\ Cg\ S\ RS\ HS\ CgS) - R(\mu\ R\ H\ Cg\ S)]$$
$$= K_{16}\ \sigma^2_{RS} + K_{17}\ \sigma^{2*}_{HS} + K_{18}\ \sigma^{2*}_{CgS} + K_{19}\ \sigma^2_{e(2)}.$$

Where $K_{16} = tr\ (X'_{RS}S_kX_{RS}) - tr\ (X'_{RS}Q_kX_{RS})$,

$K_{17} = tr\ (X'_{HS}S_kX_{HS}) - tr\ (X'_{HS}Q_kX_{HS})$,

$K_{18} = tr\ (X'_{CgS}S_kX_{CgS}) - tr\ (X'_{CgS}Q_kX_{CgS})$,

$K_{19} = rank\ X'X - rank\ X'_{FE}X_{FE} - rank\ X'_SS_kX_S$.

$$E[Y'Y - R(\mu\ R\ H\ Cg\ S\ RS\ HS\ CgS)]$$
$$= K_{20}\ \sigma^2_{e(2)}$$

where $K_{20} = N - rank\ (X'X)$.

Table 6 contains the values for the k-coefficients for the variance components from model (2) for birth weight, weaning weight and postweaning gain.

To calculate the k-coefficients for the variance component equations, traces of matrices are needed. For model (1) analyses, the following traces were calculated:

$$tr\ (X'_SS_iX_S) = tr\ (X'_{HS}S_iX_{HS}) = tr\ (X'_{CgS}S_iX_{CgS}) = \sum_l\left(\sum_{jk}N_{jkl.} - \frac{N^2_{jkl.}}{N_{jk..}}\right).$$

$$tr\ (X'_{HS}Q_iX_{HS}) = tr\ (X'_{HS}S_iX_S(X'_SS_iX_S)^-X'_SS_iX_{HS}).$$

Table 6. The k-coefficients for the variance components from the across region of the United States model for birth weight, weaning weight and postweaning gain

	Birth weight	Weaning weight	Postweaning gain
k_{11}[a]	1312.0	4694.9	973.2
k_{12}	1312.0	4694.9	973.2
k_{13}	1312.0	4694.9	973.2
k_{14}	1312.0	4694.9	973.2
k_{15}	400	1834	270
k_{16}[b]	539.1	2221.5	412.2
k_{17}	668.2	2776.9	539.7
k_{18}	1129.2	4320.5	807.4
k_{19}	368	1748	240
k_{20}[c]	1639	5612	1370

[a] $R(\mu\ R\ H\ Cg\ S\ RS\ HS\ CgS) - R(\mu\ R\ H\ Cg) = k_{11}\sigma^2_{S_{(2)}} + k_{13}\sigma^{2*}_{HS} + k_{14}\sigma^{2*}_{CgS} + k_{15}\sigma^2_{e_{(2)}}$ where σ^{2*}_{HS} and σ^{2*}_{CgS} were weighted average estimates of variance from model (1) analyses.

[b] $R(\mu\ R\ H\ Cg\ S\ RS\ HS\ CgS) - R(\mu\ R\ H\ Cg\ S) = k_{16}\sigma^2_{RS} + k_{17}\sigma^{2*}_{HS} + k_{18}\sigma^{2*}_{CgS} + k_{19}\sigma^2_{e_{(2)}}$.

[c] $Y'Y - R(\mu\ R\ H\ Cg\ S\ RS\ HS\ CgS) = k_{20}\sigma^2_{e_{(2)}}$.

$X'_{HS}S_iX_S$ = Each $H_jS_1S_1$ element = $\sum_k(N_{jk1.} - \frac{N^2_{jk1.}}{N_{jk..}})$.

Each H_jS1S1' element = $-\sum_k(\frac{N_{jk1.}N_{jk1'.}}{N_{jk..}})$.

$X'_SS_iX_S$ = Each $S1S1$ element = $\sum_{jk}(N_{jk1.} - \frac{N^2_{jk1}}{N_{jk..}})$.

Each $S1S1'$ element = $-\sum_{jk}(\frac{N_{jk1.}N_{jk1'.}}{N_{jk..}})$.

The generalized inverse of $X_SS_iX_S$ was calculated. After the appropriate matrices were created, the trace of $(X'_{HS}Q_kX_{HS})$ was computed by multiplying only those elements of $X'_{HS}S_iX_S$, $(X'_SS_iX_S)^-$ and $X'_SS_iX_{HS}$ that contributed to the diagonal elements of $X'_{HS}Q_iX_{HS}$. The diagonal elements were summed to calculate the trace.

$tr\ (X'_{CgS}Q_iX_{CgS}) = tr\ (X'_{CgS}S_iX_S(X'_SS_iX_S)^-X'_SS_iX_{CgS})$.

$X'_{CgS}S_iX_S$ = Each $Cg_{jk}S1S1$ element = $(N_{jk1.} - \frac{N^2_{jk1.}}{N_{jk..}})$.

Each $Cg_{jk}S1S1'$ element = $-(\frac{N_{jk1.}N_{jk1'.}}{N_{jk..}})$.

The trace of $X'_{CgS}Q_iX_{CgS}$ was calculated similar to the trace of $X'_{HS}Q_iX_{HS}$.

$$\text{tr}\,(X'_{Cg}S_jX_{Cg}) = \text{tr}\,(X'_{CgS}S_jX_{CgS}) = \sum_k\left(\sum_l\left(N_{jkl.} - \frac{N^2_{jkl.}}{N_{j..}}\right)\right).$$

$$\text{tr}\,(X'_{CgS}Q_jX_{CgS}) = \text{tr}\,(X'_{CgS}S_jX_{Cg}(X'_{Cg}S_jX_{Cg})^-X'_{Cg}S_jX_{CgS}).$$

$X'_{CgS}S_jX_{Cg}$ = Each $Cg_{jk}S_lCg_{jk}$ element $= \left(N_{jkl.} - \frac{N^2_{jkl.}}{N_{j..}}\right)$.

Each $CgjkSlCg_{jk'}$ element $= -\left(\frac{N_{jkl.}N_{jk'l.}}{N_{j..}}\right)$.

Each $Cg_{jk}SlCg_{j'k'}$ element $= 0$.

$X'_{Cg}S_jX_{Cg}$ = Each $Cg_{jk}Cg_{jk}$ element $= \sum_l\left(N_{jkl.} - \frac{N^2_{jkl.}}{N_{j..}}\right)$.

Each $Cg_{jk}Cg_{jk'}$ element $= -\sum_l\left(\frac{N_{jkl.}N_{jk'l.}}{N_{j..}}\right)$.

Each $Cg_{jk}Cg_{j'k'}$ element $= 0$.

The generalized inverse of $X'_{Cg}S_jX_{Cg}$ was calculated. After the appropriate matrices were created, the trace of $(X'_{CgS}Q_jX_{CgS})$ was computed by multiplying those elements of $(X'_{CgS}S_jX_S)$, $(X'_{Cg}S_jX_{Cg})^-$ and $X'_SS_jX_{CgS}$ that contributed to the diagonal elements of $(X'_{CgS}Q_jX_{CgS})$. The trace was computed by summing the diagonal elements.

For the model (2) analyses, the following traces were also calculated.

$$\text{tr}\,(X_S'S_kX_S) = \text{tr}\,(X_{RS}'S_kX_{RS}) = \text{tr}\,(X_{HS}'S_kX_{HS}) = \text{tr}\,(X_{CgS}'S_kX_{CgS})$$

$$= \sum_l\left(\sum_{ijk} N_{ijkl.} - \frac{N_{ijkl.}^2}{N_{ijk..}}\right).$$

$$\text{tr}\,(X_{RS}'Q_kX_{RS}) = \text{tr}\,(X_{RS}'S_kX_S(X_S'S_kX_S)^{-}X_S'S_kX_{RS}).$$

$$\text{tr}\,(X_{HS}'Q_iX_{HS}) = \text{tr}\,(X_{HS}'S_kX_S(X_S'S_kX_S)^{-}X_S'S_kX_{HS}).$$

$$\text{tr}\,(X_{CgS}'Q_kX_{CgS}) = \text{tr}\,(X_{CgS}'S_kX_S(X_S'S_kX_S)^{-}X_S'S_kX_{RS}).$$

$X_{RS}'S_kX_S =$ Each $R_iS_lS_l$ element $= \sum_{jk}\left(N_{ijkl.} - \frac{N_{ijkl.}^2}{N_{ijk..}}\right)$.

Each $R_iS_lS_l'$ element $= -\sum_{jk}\left(\frac{N_{ijkl'.}N_{ijkl'.}}{N_{ijk..}}\right)$.

$X_S'S_kX_S =$ Each S_lS_l element $= \sum_{ijk}\left(N_{ijkl.} - \frac{N_{ijkl.}^2}{N_{ijk..}}\right)$.

Each S_lS_l' element $= -\sum_{ijk}\left(\frac{N_{ijkl.}N_{ijkl'.}}{N_{ijk..}}\right)$.

$X_{HS}'S_kX_S =$ Each $H_{ij}S_lS_l$ element $= \sum_{k}\left(N_{ijkl.} - \frac{N_{ijkl.}^2}{N_{ijk..}}\right)$.

Each $H_{ij}S_lS_l'$ element $= -\sum_{k}\left(\frac{N_{ijkl.}N_{ijkl'.}}{N_{ijk..}}\right)$.

$X_{CgS}'S_kX_S =$ Each $Cg_{ijk}S_lS_l$ element $= \left(N_{ijkl.} - \frac{N_{ijkl.}^2}{N_{ijk..}}\right)$.

Each $Cg_{ijk}S_lS_l'$ element $= -\left(\frac{N_{ijkl.}N_{ijkl'.}}{N_{ijk..}}\right)$.

The generalized inverse of $X'_S S_k X_S$ was calculated, and the diagonal elements of $(X'_{RS} Q_k X_{RS})$, $(X'_{HS} Q_k X_{HS})$ and $(X'_{CgS} Q_k X_{CgS})$ were constructed similarly to the matrices for model (1), and the trace of each matrix was obtained.

Dickerson (1962) uses an intra-class method to estimate the average genetic correlation of sire breeding values in different environments. The intra-class correlation formula for the genetic correlation is $r_G = \frac{\sigma^2_S}{\sigma_S + \sigma^2_{SE}}$, where σ^2_S is the sire variance across environments, and σ^2_{SE} is the sire by environment interaction variance. The correlation between sire estimated progeny differences in different regions was estimated by $\frac{\sigma^2_{S(2)}}{\sigma^2_{S(2)} + \sigma^2_{RS}}$. This expression was the correlation among progeny of the same sire after accounting for herd within region by sire and contemporary group within herd by sire effects. The correlation between sire estimated progeny differences in different contemporary groups within herds and different herds within regions was estimated by $\frac{\sigma^2_{S(2)}}{\sigma^2_{S(2)} + \sigma^2_{CgS}}$ and $\frac{\sigma^2_{S(2)}}{\sigma^2_{S(2)} + \sigma^2_{CgS} + \sigma^2_{HS}}$.

Mixed model procedures were used to obtain Best Linear Unbiased Predictors (BLUP) of sire expected progeny differences (EPDs) in each of the nine regions. The model to predict EPDs within a region was:

$$Yijkl = \mu + Cg_i + S_j + CgS_{ij} + e_{ijk},$$

Y_{ijk} = the observation of the k^{th} calf of the j^{th} sire in the i^{th} contemporary group,

where μ = overall mean,

Cg_i = the fixed effect of the i^{th} contemporary group within a herd,

S_j = the random effect of the j^{th} sire,

CgSij = the random interaction of the i^{th} contemporary group within a herd and the j^{th} sire,

eijkl = random error.

The mixed model equations were:

$$\begin{bmatrix} X'X & X'Z_1 & X'Z_2 \\ Z_1'X & Z_1'Z_1+I\frac{\sigma_{e(1)}^2}{\sigma_{INT}^2} & Z_1'Z_2 \\ Z_2'X & Z_2'Z_1 & Z_2'Z_2+I\frac{\sigma_{e(1)}^2}{\sigma_{S(1)}^2} \end{bmatrix} \begin{bmatrix} B \\ CgS \\ S \end{bmatrix} = \begin{bmatrix} X'Y \\ Z_1'Y \\ X_2'Y \end{bmatrix},$$

where σ_{INT}^2 = weighted average estimate for σ_{HS}^2 plus the weighted average estimate for σ_{CgS}^2.

$\sigma_{S(1)}^2$ = the weighted average sire estimates from model (1),

$\sigma_{e(1)}^2$ = the weighted average error estimate from model (1).

The strategy used to solve the equations was:

1. Order the data by herd, contemporay group within herd and sires within contemporary group.
2. At the end of the data for a sire within a contemporary group, absorb the contemporary group within herd by sire effect into the contemporary group within herd and sire equations.
3. At the end of all data for a herd absorb the contemporary group within herd effects into the sire equations.

4. Write out all sire coefficients for a herd and repeat steps 2 and 3 for all herds and contemporary groups within herds.
5. Collect and sum like sire coefficients across herds to form the complete sire equations.
6. Solve the sire equations by an iterative process.

The product-moment and rank correlations of sire EPDs in different regions were obtained. Tests of significance for the correlation statistics were made according to procedures outlined by Steel and Torrie (1960).

The correlation of sire EPDs in different regions was also calculated using approximation procedures outlined by Everett (1983). The procedure may be used to unbiasedly approximate a genetic (co) variance using a linear adjustment of the (co) variance between estimated progeny differences of sires with progeny in two different regions. The method assumes that there is no environmental correlation between the progeny of each sire in different environments.

With the assumption that there were no environmental correlations, the following expectations hold:

$$E[\hat{u}_i'\hat{u}_i] = tr\ [I-C_i\lambda_i]\ \sigma^2_{Si}$$

$$E[\hat{u}_i\hat{u}_j] = tr\ [I-C_i\lambda_i]'[I-C_j\lambda_j]\ \sigma_{Sij}$$

where $\hat{u}_i$ and $\hat{u}_j$ are the sire EPDs in different regions,

C_i and C_j correspond to the sire portion of the inverse of the mixed model equations in each region,

$$\lambda_i = \lambda_j = \sigma_{e(1)}^2 / \sigma_{S(1)}^2 = \lambda ,$$

σ_{Si}^2 = the sire variance in the i^{th} region,

σ_{Sij} = the genetic covariance between sire EPDs in different regions.

Ignoring the off-diagonals of C_i and C_J yield the following approximations:

$$Ci \tilde{=} \text{diag} \left(\frac{1}{Mik+\lambda}\right) ,$$

$$Cj \tilde{=} \text{diag} \left(\frac{1}{Mjk+\lambda}\right) ,$$

where Mik and Mjk are the effective number of progeny for each k^{th} sire in the i^{th} or j^{th} region. Using the approximation of Ci and Cj we now have:

$$\text{diag} (I-Ci\lambda) = \text{diag} \left(\frac{M_{ik}}{Mik+\lambda}\right) = b_{ik} ,$$

and $$\text{diag} (I-Cj\lambda) = \text{diag} \left(\frac{M_{jk}}{Mjk+\lambda}\right) = bjk.$$

We now can approximate the values of σ_{Si}, σ_{Sj} and σ_{Sij} by:

$$\sigma_{Si}^2 = \hat{u}_i'\hat{u}_i / \sum_{k=1}^{qi} bik,$$

$$\sigma_{Sj}^2 = \hat{u}_j'\hat{u}_j / \sum_{k=1}^{qj} bjk,$$

$$\sigma_{Sij} = \hat{u}_i'\hat{u}_j / \sum_{k=1}^{q} bik\ bjk,$$

qi = total number of sires with progeny in the 1^{th} region,

qj = total number of sires with progeny in the j^{th} region,

q = the number of sires with progeny in both regions.

The correlation of sire EPDs in different regions was then estimated by $\sigma_{Sij} / \sigma_{Si}\sigma_{Sj}$.

Across regions, across herds within region, within herd and within contemporary group heritability (h^2) estimates were calculated according to the formulas:

$\frac{4\sigma_{S(2)}^2}{\sigma_p^2}$ = across region h^2,

$\frac{4(\sigma_{S(2)}^2 + \sigma_{RS}^2)}{\sigma_p^2}$ = across herds within a region h^2,

$\frac{4(\sigma_{S(2)}^2 + \sigma_{RS}^2 + \sigma_{HS}^2)}{\sigma_p^2}$ = within herd h^2, and

$\frac{4(\sigma_{S(2)}^2 + \sigma_{RS}^2 + \sigma_{HS}^2 + \sigma_{CgS}^2)}{\sigma_p^2}$ = within a contemporary group h^2.

$$\sigma_p^2 = \sigma_{S(2)}^2 + \sigma_{RS}^2 + \sigma_{HS}^2 \sigma_{CgS}^2 + \sigma_{e(1)}^2.$$

RESULTS AND DISCUSSION

Weaning Weight

Variance components

Table 7 contains estimates for sire, herd by sire, contemporary group within herd by sire, error and total phenotypic variances obtained from the nine within-region analyses. The weighted average estimates for each of the five variance components are also in Table 7. The average estimates for sire, herd by sire, contemporary group within herd by sire and error variances were calculated by weighting each region's variance component estimates by the degrees of freedom available for the effect, summing over all the regions and dividing the sum by the number of total degrees of freedom available across regions for each effect. The average total phenotypic variance estimate was calculated by summing the weighted averages of sire, herd by sire, contemporary group within herd by sire and error variance estimates.

Estimates across regions for sire, region by sire, average herd within region by sire, average contemporary group within herd by sire, average error and total phenotypic variances are presented in Table 8. The weighted average herd within region by sire, contemporary group within herd by sire and error from the nine within-region analyses were considered the most appropriate estimates due to the hierarchal

Table 7. Within region of the United States variance component estimates for weaning weight (kg^2)

Region	$\sigma^2_{S_1}$[a]	σ^2_{HS}	σ^2_{CgS}	$\sigma^2_{e_1}$	σ^2_p[b]
Northeast	25	2	47	443	516
Cornbelt	19	26	-9	575	611
South	13	29	61	485	588
Gulf Coast	40	6	-27	493	513
Upper Plains	13	13	14	430	470
Lower Plains	22	-2	44	509	572
Rocky Mts.	-4	-2	78	535	611
Desert S.W.	44	-3	-76	497	461
Pacific	70	-7	33	445	541
Weighted[c] average	22	13	24	490	549

[a] $\sigma^2_{S_1}$ = sire variance, σ^2_{HS} = herd by sire variance, σ^2_{CgS} = contemporary group within herd by sire variance, $\sigma^2_{e_1}$ = error variance and σ^2_p = total phenotypic variance.

[b] $\sigma^2_p = \sigma^2_{S_1} + \sigma^2_{HS} + \sigma^2_{CgS} + \sigma^2_{e_1}$.

[c] Weighted average for each variance component was found by weighting each region's estimate by the degrees of freedom available for the random effect, summing over all nine regions and dividing the sum by the total degrees of freedom across regions.

Table 8. Across regions of the United States variance component and heritability estimates for weaning weight (kg^2)

Variance Components					
$\sigma^2_{S_2}$[ab]	σ^2_{RS}	σ^2_{HS}	σ^2_{CgS}	$\sigma^2_{e_1}$	σ^2_p[c]
14	8	13	24	490	549
86	217	582	2764	13633	

Heritability[d]			
h^2_{AR}	h^2_{AH}	$h^2_{w/H}$	$h^2_{w/Cg}$
.11	.17	.28	.46

[a] $\sigma^2_{S_2}$ = across region sire variance, σ^2_{RS} = region by sire variance, σ^2_{HS} = herd within region by sire variance, σ^2_{CgS} = contemporary group within herd by sire variance, $\sigma^2_{e_1}$ = error variance and σ^2_p = total phenotypic variance.

[b] The variance estimate is listed first and the number of degrees of freedom available for the estimation of each corresponding random effect is listed below the variance estimate.

[c] $\sigma^2_p = \sigma^2_{S_2} + \sigma^2_{RS} + \sigma^2_{HS} + \sigma^2_{CgS} + \sigma^2_{e_1}$.

[d] h^2_{AR} = across region heritability, h^2_{AH} = across herd within region heritability, $h^2_{w/H}$ = within herd heritability and $h^2_{w/Cg}$ = within contemporary group heritability.

structure of the data, the procedures used to create herd by sire and contemporary group within herd by sire cells in the within-region analyses and the large numbers of records available for their estimation.

The magnitude of the herd within region by sire and contemporary group within herd by sire variances expressed as a percentage of the across-region sire variance was 93% and 171%, respectively. The magnitude of these interaction variance components indicated that they should be considered as important sources of variation in a mixed model sire evaluation of weaning weight for the Polled Hereford breed.

The estimates of herd within region by sire and contemporary group within herd by sire interactions were due to true biological causes and due to an extra correlation between progeny of the same sire. This extra correlation could be attributed to nonrandom mating of sires and/or preferential treatment of dams and/or progeny. In Polled Hereford field data sire evaluations since 1982, a contemporary group within herd by sire effect was included in the model. The ratio $\sigma^2_e/\sigma^2_{Int}$, where σ^2_{Int} was the sum of the herd within region by sire and contemporary group within herd by sire variances and σ^2_e was random error variance, was used to account for the distribution of the contemporary group within herd by sire random effects. The absorption of contemporary group within herd by sire effects into contemporary group within herd effects sets an upper limit equal to $\sigma^2_e/\sigma^2_{Int}$ for the maximum number of progeny a sire can receive credit for in a contemporary group. This technique forces a sire to have progeny spread across a number of contemporary groups to achieve a high enough accuracy to allow consideration for inclusion in the breed's sire

summary. A sire was also required to have progeny in at least two herds before his expected progeny difference (EPD) would be reported in the American Polled Hereford Association Sire Summary (1982). Forcing a sire's progeny to be spread over many contemporary groups and over at least two herds was an attempt to reduce the effects of nonrandom mating and preferential treatment that was probably practiced in many herds.

The region by sire variance component estimates expressed as a percentage of the across region sire variance was 57%. Nunn et al. (1978) and Buchanan and Nielson (1979) found percentages of 28% and 29%, respectively; however, Tess et al. (1979) found that the region by sire variance was 50% as large as the sire variance. The magnitude of the region by sire variance component estimate indicated that consideration should be given to procedures that account for region by sire effects.

The estimate for the across-region sire variance plus the region by sire variance was equal to the weighted average within-region sire variance from Table 7. This was expected due to the hierarchal structure of the fixed effects of region, herd within region and contemporary group within herd.

The across-region sire variance and the average within-region error variance from the nine region analyses were 2.6% and 89.2%, respectively, of the total phenotypic variance. Massey and Benyshek (1981) found that the sire variance was 2.4%, and the error variance was 97.6% of the total variance; however, they did not attempt to estimate any environment by sire variance components which, consequently, contributed to error variance.

The estimate of total phenotypic variance was less than the average phenotypic variance found by Woldehawariat et al. (1977). However, reports of phenotypic variance for weaning weight are variable. Bauer et al. (1978) found a phenotypic variance of 49 kg^2, while Pabst et al. (1977) found a phenotypic variance of 2926 kg^2. The phenotypic variance found in this study was similar to the 537 kg^2 found by Lehman et al. (1961) and 566 kg^2 found by Nunn et al. (1978).

Negative estimates of variance components can occur when using Henderson Method 3 estimation procedures. Negative estimates for sire, herd by sire and contemporary group within herd by sire variance components were found in some of the within-region analyses. It is essential that enough filled contemporary group within herd by sire and herd by sire cells are available to reduce the sampling variance when estimating these variance components. In field data, it may be difficult to obtain enough filled cells to successfully reduce the sampling variance to estimate the variance components with a high degree of precision. Table 9 contains the degrees of freedom available for each random effect from the nine within-region analyses for weaning weight. The majority of the negative estimates for herd by sire and contemporary group within herd by sire variances occurred in those regions with the fewest degrees of freedom. The Cornbelt region was one notable exception. It had the second highest number of contemporary group within herd by sire degrees of freedom, yet the estimated variance for the contemporary group within herd by sire effects were negative. This further illustrated the need for adequate amounts of data to

Table 9. The degrees of freedom available for the random effects from the within region of the United States analyses for weaning weight

Region	Sire	Herd by sire	Cont. group by sire	Error
Northeast	53	83	431	1465
Cornbelt	124	180	528	3092
South	33	35	185	864
Gulf Coast	26	30	153	698
Upper Plains	105	124	646	3679
Lower Plains	63	63	431	1884
Rocky Mts.	24	32	198	783
Desert S.W.	9	9	55	285
Pacific	26	26	137	883
Total	463	582	2764	13633

effectively reduce sampling variances.

There were also no rules for selecting those combinations of reductions which would yield variance components with the lowest sampling variances. The reductions in this study were chosen because they were computationally feasible and allowed for variance component estimation free of fixed and certain random effects.

A major disadvantage with Henderson Method 3 variance estimation procedures was the need for generalized inverses of matrices. When very large models containing a large number of effects are used, calculating a large generalized inverse could become a problem. Sires contributing to the within-region analyses had progeny in common with another sire in at least two herds within the region, at least two contemporary groups within each herd, and two or more progeny in half the contemporary groups. Editing the data in this manner significantly reduced the sire matrices and allowed for the direct calculation of generalized inverses. The hierarchal structure of the fixed effects kept the size of the contemporary group within herd matrices to a manageable size and allowed for the calculation of each generalized inverse for contemporary groups within a herd independently for each herd.

A problem that existed in this study was a possible bias in the variance component estimates due to the original assumption that the covariances between the random effects in the model were zero. Nonrandom mating of sires was probably occurring in most herds and may give rise to some covariance terms between the random effects. The existence of these covariance terms was probably the reason why the contemporary group within herd by sire and herd within region by sire variance component estimates

were larger for weaning weight.

Heritability

The across regions, across herds within a region, within herd and within contemporary group heritability estimates for weaning weight are presented in Table 8. When important environment by sire interactions exist, heritability estimates over wide ranges of environments and locations should decrease. The heritabilities in Table 8 show this decreasing trend. Estimated heritability within contemporary group was substantially larger than across regions.

The within herd heritability estimate of .28 was similar to the average estimate of .31 reported by Woldehawariat et al. (1977). Most literature estimates of heritability have been from within herd investigations and have not benefited from extensive performance data files where sires are distributed across herds and regions.

The heritability estimate across herds within a region of .17 was higher than the .09 found by Tess et al. (1979) and lower than the .27 and .24 found by Buchanan and Nielson (1979). Estimated heritability across regions was .11. This was similar to the average of across region estimates from the literature (.14) which were summarized in Table 2.

Prior to the opportunity to characterize the variability in field data files, it was necessary to use parameter estimates available from the literature in national sire evaluations. Consequently, heritability was assumed to be .30 for weaning weight in previous Polled Hereford National Sire Evaluations. Since the data represent progeny distributed across regions, an estimate across regions and herds would seem more appropriate than the previous within-herd estimates of heritability from the litera-

ture. The ultimate impact of using the heritability estimate of .11 found in this study in future Polled Hereford National Sire Evaluations instead of the previous estimate of .30 would be the increased regression of sire EPDs. As a result, if all other parameters in the model remained constant, more progeny per sire would be required in future sire evaluations to achieve the level of accuracy used as a criteria for listing in the Polled Hereford Sire Summary. The spread of EPDs would also be less at lower heritabilities due to increased regression.

Correlation of sire EPDs across environments

Dickerson (1962) used an intra-class correlation method to estimate the genetic correlation between genotypes in different environments. The estimated genetic correlation for the EPDs of the same sire in different regions was .64. This value expresses the correlation among progeny of the same sire after accounting for contemporary group within herd by sire and herd within region by sire effects. The average genetic correlation estimate of weaning weight sire EPDs across contemporary groups within herds and herds within region was .37 and .27, respectively. Robertson (1959) suggested that an estimated genetic correlation of .80 or lower would indicate that some rank changes were occurring among genotypes in different environments. The genetic correlations of .27 and .37 for the EPDs of sires in different herds within regions and contemporary groups within herds indicated that substantial rank changes of sire EPDs in different herds within regions and contemporary groups within herds were occurring. It was apparent that the effects of herd within region by sire and contemporary group within herd by

sire interactions were significant, and methods of accounting or controlling these interactions are essential. At the present time, these interactions are considered as random effects and are included in the National Polled Hereford Sire Evaluation model, and an effort is made to control their effect on sire EPDs by the use of the ratio $^{2}_{e}/^{2}_{Int}$. The effects of nonrandom mating and/or preferential treatment are major causes of significant estimated effects for these two interactions. Methods suggested by Wilson (1983) and Zollinger and Nielson (1983) would adjust calf weaning records for dam breeding value in addition to age of dam and 205-day adjustments. With the development of within-herd evaluations tied into national sire evaluation, it may be possible to account for the effects of nonrandom mating and/or preferential treatment including dam effects in the sire evaluation model.

A main objective of this study was to determine the effect of region by sire interactions on the correlation of sire EPDs across regions. Unlike herd within region by sire and contemporary group within herd by sire effects which are too numerous, the discovery of significant region by sire effects may make it necessary to conduct sire analyses separately for some regions or to calculate some region by sire effects to adjust the EPDs.

Table 10 contains product-moment and rank correlations of EPDs for sires with progeny in each of two regions. Both correlations were similar in value across the regions. The weighted average product-moment and rank correlations from Table 10 were .55. Rank changes appear to be occurring; however, since the EPDs were regressed for incomplete heritabilities, the correlations between sire EPDs in different regions were also a function of the number of progeny a sire had in each region. If a sire had many proge-

Table 10. Product-moment and rank correlations of weaning weight expected progeny differences of sires with progeny in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.59[a]	.65	.36	.64	.67	.56	.46	.47
	.54[b]	.63	.44	.63	.66	.57	.46	.55
	273[c]	260	120	234	240	139	121	128
Cornbelt		.59	.45	.50	.63	.48	.52	.54
		.56	.49	.50	.59	.49	.50	.55
		272	128	234	344	136	113	133
South			.51	.64	.74	.57	.52	.59
			.53	.66	.75	.60	.52	.64
			291	175	373	147	123	156
Gulf Coast				.50	.58	.39	.49	.38
				.49	.57	.42	.44	.40
				87	185	80	71	87
Upper Plains					.66	.39	.40	.50
					.67	.38	.36	.62
					242	153	91	90
Lower Plains						.60	.49	.54
						.64	.43	.59
						175	141	145
Rocky Mts.							.38	.63
							.39	.61
							133	124
Desert S.W.								.34
								.28
								169

[a]Product-moment correlation.

[b]Rank correlation.

[c]The number of sires with progeny in the two regions.

ny in one region and few progeny in the other, the correlation between his EPDs may not be high simply because his EPD was regressed less in one region than the other.

A fundamental problem in the analysis of field data is that the true EPD for a sire is not known. Further, the error of prediction is influenced by the number of progeny of a sire and varies from one sire to another. Two alternatives were considered to minimize the effect of varying number of progeny which relates directly to prediction error. First, product-moment and rank correlations were estimated between EPDs of sires with an expected progeny number (EPN) greater than or equal to 20 within regions. The effective progeny number was the number of progeny of a sire that was fairly compared within contemporary groups with progeny of other sires and was always considerably less than the actual number of progeny. By limiting the data to sires with smaller prediction errors (high accuracy), the correlation should be more effective in reflecting the true relationship between sire EPDs in different regions. Table 11 presents the product-moment and rank correlations among sires meeting this criteria in each of two regions. The rank correlations were slightly greater than or equal to the product-moment correlations for half of the region by region combinations. Again, the rank and product-moment correlations appear to be very similar across regions. Table 12 contains the weighted average product-moment and rank correlations of sire EPDs for each region. The EPDs used in this table were from sires that had 20 or greater EPN in each of two regions. From this table, it appeared that the Gulf Coast and the Lower Plains EPDs were likely to be highly correlated

Table 11. Product-moment and rank correlations of weaning weight expected progeny differences of sires with ≥20 expected progeny number in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.67[a]	.43	.70	.73	.87	.59	.56	.70
	.72[b]	.39	.50	.71	.88	.60	.60	.71
	16[c]	19	3	7	10	5	5	7
Cornbelt		.65	.90	.52	.67	.53	.47	.63
		.70	.86	.46	.63	.30	.30	.74
		22	7	11	17	5	5	11
South			.85	.23	.82	.65	.17	.78
			.86	.14	.71	.70	.12	.78
			13	6	23	9	9	19
Gulf Coast				-.97	.84	.85	1.00	.29
				-1.00	.83	.80	1.00	.50
				3	9	4	2	3
Upper Plains					.77	.89	--	.64
					.85	.90	--	.80
					11	5	1	4
Lower Plains						.61	.44	.38
						.79	.54	.17
						10	6	9
Desert S.W.							.23	.56
							.50	.55
							7	14
Rocky Mts.								.23
								.60
								6

[a]Product-moment correlation.

[b]Rank correlation.

[c]The number of sires with ≥20 expected progeny number in the two region.

Table 12. Average region product-moment and rank correlations of weaning weight expected progeny differences of sires with ≥20 expected progeny number in each of two regions of the United States

Region[a]	Product-moment correlation	Rank correlation	Total number of sires
Northeast	.62[ce]	.62[ce]	72
Cornbelt	.64[ce]	.65[ce]	94
South	.64[ce]	.62[ce]	120
Gulf Coast	.76[d]	.76[d]	44
Upper Plains	.58[c]	.58[cef]	49
Lower Plains	.71[de]	.69[de]	95
Rocky Mts.	.57[c]	.64[ce]	59
Desert S.W.	.31	.41[f]	42
Pacific	.60[c]	.63[ce]	73
Weighted average[b]	.63[c]	.63[ce]	320

[a]Each region correlation was calculated by weighting each region by region correlation by the number of sires, summing across the region by region combinations that contain the region of interest and dividing the sum by the total number of sires.

[b]The weighted average was calculated by weighting each region by region correlation by the number of sires, summing across all region by region combinations and dividing the sum by the total number of sires.

[c,d,e,f]All correlations with like subscripts were not significant at ($p<.05$).

with other regions; the Northeast, Cornbelt, South, Lower Plains, Rocky Mountains and the Pacific EPDs were intermediately correlated with other regions; and the Desert Southwest EPDs were poorly correlated with other regions. The weighted average product-moment and rank correlation from Table 12 were both .63. There appeared to be rank changes of sire EPDs across regions, with the Desert Southwest having the most severe rank change of sire EPDs compared to the other regions.

A definite problem with using those sires with 20 or greater EPN to calculate correlations was that the number of sires was severely reduced. The Gulf Coast and the Desert Southwest were the two extremes for correlations from Table 12. These two regions also had the least number of progeny available to estimate the correlations. A second method was used to calculate the correlation between sire EPDs in different regions. The method, explained by Everett (1983), approximated the genetic variances and covariances of EPDs in different regions and used the traces of the inverse of sire coefficient matrices to account for the number of progeny that contributed to each sire's estimate. Table 13 presents the correlations for sire EPDs with progeny in each of two regions using the approximation method explained by Everett (1983). The correlations from Table 13 appeared to be less variable from region to region than those correlations of EPDs for sires with greater than or equal to 20 EPN from Table 11. This was probably due to the inclusion of more information per region.

Table 14 contains the weighted average correlations of EPDs for each region using the approximation method. The Upper Plains region appeared to

Table 13. Estimates of weaning weight genetic correlations of sire expected progeny differences of sires with progeny in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.60[a] 273[b]	.63 260	.52 120	1.00 234	.73 240	.81 139	.57 121	.51 128
Cornbelt		.44 272	.47 128	.69 234	.64 344	.73 136	.57 113	.48 133
South			.49 291	.93 175	.72 373	.74 147	.51 123	.43 156
Gulf Coast				.96 87	.64 185	.52 80	.69 71	.45 87
Upper Plains					.90 242	.68 153	.69 91	.61 90
Lower Plains						.68 175	.54 141	.53 145
Rocky Mts.							.54 133	.66 124
Desert S.W.								.39 169

[a]The genetic correlation estimates for EPDs of sires with progeny in the two different regions using approximation procedures explained by Everett (1983).

[b]The number of sires with progeny in the two regions.

Table 14. Average region estimates of weaning weight genetic correlations of sire expected progeny differences of sires with progeny in each of two regions of the United States

Region[a]	Correlation[b]	Total number of sires
Northeast	.69	1515
Cornbelt	.58	1633
South	.61	1797
Gulf Coast	.57	1049
Upper Plains	.83	1306
Lower Plains	.69	1845
Rocky Mts.	.67	1087
Desert S.W.	.54	962
Pacific	.50	1032
Weighted average[c]	.64	6113

[a]Each region correlation was calculated by weighting each region by region correlation by the number of sires, summing across the region by region correlations that contain the region of interest and dividing the sum by the total number of sires.

[b]The genetic correlation estimates use approximation procedures explained by Everett (1983).

[c]The weighted average was calculated by weighting each region by region correlation by the number of sires, summing across all region by region combinations and dividing the sum by the total number of sires.

have EPDs that were highly correlated with EPDs in other regions. This was probably due to the fact that the estimated variance of sire EPDs within the Upper Plains region was smaller than the estimated variances of sire EPDs within other regions. This indicated that breeders in the Upper Plains region were using similar genetic types of sires for weaning weight, and these sires responded genetically similar in other environments. The EPDs for the Gulf Coast region were not as highly correlated with the other regions in Table 14 compared to Table 12. The Desert Southwest and the Gulf Coast were regions with radically different types of environments than most of the other regions in the study; therefore, if significant region by sire interactions exist, it is likely that they would involve these regions. These two regions had lower correlations than all the other regions except the Pacific. The low correlation estimate for the Pacific region may be due to the moderate type of environment that exists in this region which tends to place less stress on animals, and differences between sires may not be as evident. The EPDs within the Pacific region, similar to the Upper Plains, did not show a great deal of variation; however, the sire's progeny did not perform similarly when placed in other environments. The Northeast, Cornbelt, South, Lower Plains and Rocky Mountains EPDs exhibited a great deal of variation within each region. This may indicate that there was a wide variety of selection programs occurring in these regions, or that the regions had a great deal of environmental variation within them.

The average correlations of EPDs across regions from the intra-class correlation method, the product-moment method for sires with greater than or equal to 20 EPN and the approximation method were .64, .63 and .64, respectively. There appears to be rank changes of sire EPDs across regions. With region by sire variance more than half the size of the sire variance and the occurrence of low correlations of EPDs across some of the regions, it may be necessary to evaluate sires separately for some regions or to estimate certain region by sire effects.

Birth Weight and Postweaning Gain

Variance components

Tables 15 and 16 contain the within-region sire, herd by sire, contemporary group within herd by sire, error and total phenotypic variance component estimates for birth weight and postweaning gain, respectively. The across region sire, region by sire, weighted average herd within region by sire, weighted average contemporary group within herd by sire, weighted average error and total phenotypic variance estimates are presented in Table 17.

There were large negative region by sire variance estimates for birth weight and postweaning gain. Also, every within-region analysis for birth weight produced at least one negative variance estimate for sire, herd by sire or contemporary group within herd by sire. Six of the nine within-region analyses for postweaning gain contained at least one negative

Table 15. Within region of the United States variance component estimates for birth weight (kg^2)

Region	$\sigma^2_{S_1}$[a]	σ^2_{HS}	σ^2_{CgS}	$\sigma^2_{e_1}$	σ^2_p[b]
Northeast	0.3	0.1	-0.1	10.2	10.5
Cornbelt	0.5	-0.3	0.5	14.2	14.9
South	-0.3	1.6	3.9	10.4	15.6
Gulf Coast	3.5	-1.0	1.2	14.7	18.4
Upper Plains	-0.9	1.8	0.5	5.5	6.9
Lower Plains	1.5	-2.0	3.3	7.4	10.2
Rocky Mts.	0.3	-2.2	5.2	11.0	14.3
Desert S.W.	-2.8	3.8	4.4	13.8	19.2
Pacific	-0.8	-1.1	4.8	13.6	16.5
Weighted mean[c]	0.4	-0.1	0.9	12.2	13.4

[a] $\sigma^2_{S_1}$ = sire variance, σ^2_{HS} = herd by sire variance, σ^2_{CgS} = contemporary group within herd by sire variance, $\sigma^2_{e_1}$ = error variance and σ^2_p = total phenotypic variance.

[b] $\sigma^2_p = \sigma^2_{S_1} + \sigma^2_{HS} + \sigma^2_{CgS} + \sigma^2_{e_1}$.

[c] Weighted mean for each variance component was found by weighting each region's estimates by the degrees of freedom available for the random effect, summing over all nine regions and dividing the sum by the total degrees of freedom.

Table 16. Within region of the United States variance component estimates for postweaning gain (kg^2)

Region	$\sigma^2_{S_1}$[a]	σ^2_{HS}	σ^2_{CgS}	$\sigma^2_{e_1}$	σ^2_p[b]
Northeast	31	-20	136	398	545
Cornbelt	29	-14	-13	458	460
South	-107	153	58	454	558
Gulf Coast	19	7	129	380	535
Upper Plains	15	3	12	318	348
Lower Plains	-2	9	27	370	404
Rocky Mts.	1	29	81	433	544
Desert S.W.	33	-103	323	438	691
Pacific	-38	50	17	465	494
Weighted mean[c]	9	5	44	417	475

[a] σ^2_S = sire variance, σ^2_{HS} = herd by sire variance, σ^2_{CgS} = contemporary group within herd by sire variance, $\sigma^2_{e_1}$ = error variance and σ^2_p = total phenotypic variance.

[b] $\sigma^2_p = \sigma^2_{S_1} + \sigma^2_{HS} + \sigma^2_{CgS} + \sigma^2_{e_1}$.

[c] Weighted mean for each variance component was found by weighting each region's estimate by the degrees of freedom available for the random effect, summing over all nine regions and dividing the sum by the total degrees of freedom.

Table 17. Across regions of the United States variance component and heritability estimates for birth weight (kg^2) and post-weaning gain

	Variance Components					
Trait	$\sigma^2_{S_2}$[a]	σ^2_{RS}	σ^2_{HS}	σ^2_{CgS}	$\sigma^2_{e_1}$	σ^2_p[b]
Birth weight	0.7	-0.7	-0.1	0.9	12.2	13.0
Postweaning gain	36	-43	5	44	417	501

	Heritability			
Trait	h^2_{AR}[c]	h^2_{AH}	$h^2_{w/H}$	$h^2_{w/Cg}$
Birth weight	.22	0.0	-0.3	.25
Postweaning gain	.29	-0.6	-0.2	.36

[a] $\sigma^2_{S_2}$ = across region sire variance, σ^2_{RS} = region by sire variance, σ^2_{HS} = herd within region by sire variance, σ^2_{CgS} = contemporary group within herd by sire variance, $\sigma^2_{e_1}$ = error variance and σ^2_p = total phenotypic variance.

[b] $\sigma^2_p = \sigma^2_{S_2} + \sigma^2_{RS} + \sigma^2_{HS} + \sigma^2_{CgS} + \sigma^2_{e_1}$.

[c] h^2_{AR} = across region heritability, h^2_{AH} = across herd within a region heritability, $h^2_{w/H}$ = within herd heritability and $h^2_{w/Cg}$ = within contemporary group heritability.

variance estimate. Tables 18 and 19 contain the degrees of freedom available for each random effect from the within region analyses for birth weight and postweaning gain, respectively. Comparison of the degrees of freedom available from the within region analyses for weaning weight in Table 9 and those for birth weight and postweaning gain from Tables 18 and 19 indicated that the variance components for weaning weight were probably estimated with less sampling error than those of birth weight and postweaning gain due to the greater amount of data available for weaning weight. The largest negative estimate for the contemporary group within herd by sire variance from the within-region weaning weight analyses had 55 degrees of freedom. Seven of the birth weight regions and four of the postweaning gain regions had less than 55 degrees of freedom available for the contemporary group within herd by sire effect. There were also several regions that contained less than 26 degrees of freedom for the herd by sire effect for birthweight and postweaning gain. The largest negative herd by sire variance estimate from the within-region analyses for weaning weight contained only 26 degrees of freedom for the herd by sire effects. Table 20 presents the total degrees of freedom available for the random effects of sire, region by sire, herd within region by sire, contemporary group within herd and error effects that corresponded to the across-region variance component estimates for weaning weight, birth weight and postweaning gain. There were more than three times as many contemporary groups within herd by sire degrees of freedom available for weaning weight compared to birth weight and postweaning gain. There were also three times

Table 18. The degrees of freedom available for the random effects from the within region of the United States analyses for birth weight

Region	Sire	Herd by sire	Cont. group by sire	Error
Northeast	23	33	181	674
Cornbelt	92	123	315	1658
South	6	6	38	129
Gulf Coast	5	5	23	184
Upper Plains	13	13	40	316
Lower Plains	5	5	20	75
Rocky Mts.	1	1	5	23
Desert S.W.	2	2	10	108
Pacific	5	4	22	107
Total	152	192	654	3274

Table 19. The degrees of freedom available for the random effects from within region of the United States analyses for postweaning gain

Region	Sire	Herd by sire	Cont. group by sire	Error
Northeast	22	26	151	550
Cornbelt	77	97	268	1487
South	10	10	45	269
Gulf Coast	8	7	37	116
Upper Plains	17	17	68	801
Lower Plains	16	13	62	399
Rocky Mts.	9	10	46	338
Desert S.W.	1	1	5	45
Pacific	19	20	82	783
Total	9	202	764	4788

Table 20. The degrees of freedom available for the random effects from the across region analyses for birth weight, weaning weight and postweaning gain

Effect	Birth weight	Weaning weight	Postweaning gain
Sire	32	86	30
Region by sire	49	217	45
Herd by sire	192	582	201
Cont. group by sire	654	2764	764
Error	3274	13633	4788

as many herd by sire and four times as many region by sire degrees of freedom available for weaning weight compared to birth weight and postweaning gain. There appears to have been insufficient contemporary group within herd by sire, herd within region by sire and region by sire cells to reduce sampling variance enough to obtain good variance component estimates.

Although large negative region by sire variance components indicated that sampling variances were large, the contemporary group within herd by sire variance component estimate for birth weight and postweaning gain was over 1.2 times the size of the sire variance. The size of the contemporary group within herd by sire variances for birth weight and postweaning gain indicated that the contemporary group within herd by sire effects should still be included in future sire evaluations of birth weight and postweaning gain for the Polled Hereford breed.

The phenotypic variance for birth weight from Table 17 was larger than the average estimate reported by Woldehawariat et al. (1977). Pabst et al. (1977) found a phenotypic variance for birth weight of 42.3 kg^2, and Willis and Wilson (1974) found a phenotypic variance for birth weight of 1.9 kg^2. Anderson et al. (1974) and Koch et al. (1973) found phenotypic variances for birth weight of 12.1 kg^2 and 13.7 kg^2, respectively. The phenotypic variance estimate for postweaning gain reported in Table 17 was similar to the 491 kg^2 found by Koch et al. (1973).

Heritability

Heritability estimates across regions, across herds within a region, within a herd and within a contemporary group for birth weight and postweaning gain are presented in Table 17. The heritabilities were estimated using variance component estimates. These estimates were probably not a reflection of the true additive genetic variation for these traits in the Polled Hereford breed. The data available on these two traits were sparse, and future data sets should have more information and thus yield better estimates of variance components and heritabilities.

Correlation of sire EPDs across environments

Genetic correlations among sire EPDs using the intra-class correlation methods were inaccurately estimated due to the sparseness of data for birth weight and postweaning gain. The genetic correlation among sire EPDs across herds within a region was .47 and .42 for birth weight and postweaning gain, respectively. There was no evidence that the herd within region by sire interaction was important for either trait; however, the contemporary group within herd by sire variance was twice the size of the sire variance, and the correlations indicated that significant rank changes among sire EPDs were occurring across contemporary groups. These results

indicated that the contemporary group within herd by sire interaction effect should be included in future sire evaluation models for birth weight and postweaning gain for the Polled Hereford breed.

Product-moment and rank correlations of EPDs for birth weight of sires with progeny in two different regions are presented in Table 21. Nine of the region by region combinations either had negative product-moment or rank correlations. The weighted average product-moment correlation from Table 21 was .21, and the weighted average rank correlation was .20.

Corresponding product-moment and rank correlations for postweaning gain are in Table 22. The weighted average product-moment and rank correlations from Table 22 for postweaning gain were both .32.

There was insufficient progeny available for birth weight and postweaning gain to examine correlations of EPDs for sires with greater than or equal to 20 EPN in each of two regions. Table 23 presents the product-moment and rank correlations of EPDs for birth weight of sires with 10 or greater EPN in each of two regions. The weighted product-moment and rank correlations from Table 23 for birth weight were .35 and .37, respectively.

Table 24 reports the product-moment and rank correlations of EPDs for postweaning gain of sires with 10 or greater EPN in each of two regions. The weighted average product-moment and rank correlation from Table 24 for postweaning gain .21 and .20, respectively.

Table 25 reports correlations for birth weight EPDs using the approximation method explained by Everett (1983). The region by region correlations for birth weight ranged from -.36 for the Gulf Coast by Pacific

Table 21. Product-moment and rank correlations of birth weight expected progeny differences of sires with progeny in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.10[a]	.37	-.06	.00	.09	.25	.44	.36
	-.01[b]	.35	-.05	.21	.04	.19	.52	.30
	144[c]	122	48	75	106	75	56	80
Cornbelt		.31	.36	.06	.39	.24	.07	-.03
		.27	.36	.10	.32	.17	-.09	-.04
		145	54	68	151	69	53	80
South			.42	.28	.25	.06	.04	.40
			.51	.34	.25	.05	-.07	.38
			94	56	133	63	44	84
Gulf Coast				.21	.50	.17	-.13	-.22
				,24	.43	.15	-.18	-.15
				27	46	25	22	34
Upper Plains					.16	.37	.29	-.14
					.19	.44	.31	-.08
					63	65	43	50
Lower Plains						.28	.25	.10
						.23	.16	.13
						73	52	70
Rocky Mts.							.42	-.13
							.39	-.26
							66	69
Desert S.W.								.20
								.26
								74

[a]Product-moment correlation.

[b]Rank correlation.

[c]The number of sires with progeny in the two regions.

Table 22. Product-moment and rank correlations of postweaning gain expected progeny differences of sires with progeny in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.20[a]	.32	.46	.46	.42	.45	.49	.31
	.24[b]	.33	.46	.52	.44	.53	.29	.37
	145[c]	125	60	113	145	83	73	85
Cornbelt		.16	.20	.08	.43	.47	.20	.24
		.17	.21	.02	.44	.33	-.03	.26
		137	59	121	183	65	69	84
South			.32	.32	.35	.50	.22	.34
			.25	.41	.40	.49	.19	.37
			122	83	170	79	67	99
Gulf Coast				.52	.39	.43	.37	.52
				.68	.38	.36	.28	.46
				41	81	37	37	39
Upper Plains					.23	.30	.10	.34
					.27	.40	.18	.29
					138	85	48	56
Lower Plains						.41	.14	.17
						.48	.00	.17
						106	78	93
Rocky Mts.							.23	.41
							.11	.46
							76	86
Desert S.W.								.31
								.27
								97

[a]Product-moment correlation.

[b]Rank correlation.

[c]The number of sires with progeny in the two regions.

Table 23. Product-moment and rank correlations for birth weight expected progeny differences of sires with ≥10 expected progeny number in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.45[a]	.24	--	-.31	.25	.87	.89	.23
	.35[b]	.42	--	-.30	.50	.89	.90	.19
	18[c]	20	1	5	8	7	5	7
Cornbelt		.35	.53	-.42	.69	.93	.47	-.16
		.26	.40	.14	.61	.93	.18	-.19
		26	4	6	17	7	9	11
South			.51	.59	.10	.10	.48	.67
			.70	.40	.08	.58	.43	.71
			5	4	13	8	10	14
Gulf Coast				1.00	.89	.97	.93	--
				1.00	.50	1.00	1.00	--
				2	3	3	3	1
Upper Plains					-.36	-.56	-.100	-.62
					-.30	-.54	-.100	-.80
					5	6	2	5
Lower Plains						.42	.32	.14
						.24	-.20	.14
						8	5	6
Rocky Mts.							.73	.36
							.72	.19
							9	10
Desert S.W.								.70
								.50
								5

[a]Product-moment correlation.

[b]Rank correlation.

[c]The number of sires with ≥10 expected progeny number in the two regions.

Table 24. Product-moment and rank correlations for postweaning gain expected progeny differences of sires with ≥10 expected progeny number in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.38[a]	.56	-1.00	-.94	-.48	.92	.15	.61
	.30[b]	.44	-1.00	-1.00	-.60	.89	-.54	.43
	11[c]	15	2	3	6	6	6	10
Cornbelt		.47	.15	.36	.35	1.00	.80	.47
		.44	-.03	.48	.13	1.00	.40	.50
		22	6	11	15	4	5	12
South			.20	-.09	.04	.74	.56	.58
			.11	.20	.03	.77	.46	.44
			7	4	16	6	7	17
Gulf Coast				--	-.18	1.00	--	.92
				--	-.10	1.00	--	.80
				0	5	2	1	4
Upper Plains					.64	-.54	--	.62
					.50	-.49	--	.50
					7	6	1	3
Lower Plains						.14	.31	.24
						.31	.37	.10
						11	6	13
Rocky Mts.							.72	.39
							.83	.37
							6	15
Desert S.W.								.47
								.22
								10

[a]Product-moment correlation.

[b]Rank correlation.

[c]The number of sires with ≥10 expected progeny number in the two regions.

Table 25. Estimates of birth weight genetic correlations of sire expected progeny differences of sires with progeny in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.09[a] 144[b]	.22 122	.01 48	.08 75	.09 106	.34 75	.45 56	.38 80
Cornbelt		.23 145	.67 54	.32 68	.35 151	.39 69	.11 53	-.08 80
South			.44 94	.46 56	.28 133	.18 63	.05 44	.23 84
Gulf Coast				.69 27	.69 46	.46 25	-.20 22	-.36 34
Upper Plains					.27 63	.63 65	.47 43	-.28 50
Lower Plains						.31 73	.30 52	.07 70
Rocky Mts.							.36 66	-.20 69
Desert S.W.								.24 74

[a]The genetic correlation estimates for EPDs of sires with progeny in two different regions using approximation procedures explained by Everett (1983).

[b]The number of sires with progeny in the two regions.

correlation to .69 for the Gulf Coast by Lower Plains correlation. There were five negative correlations, with the Pacific region being involved in four of the five. Table 26 presents the weighted average region estimates for birth weight from Table 25. The Pacific region had the lowest (.05) average correlation, and the Gulf Coast had the highest (.34). The low average correlations for each region indicated that severe rank changes were occurring for birth weight EPDs across nearly every region of the United States.

Table 27 reports correlations for postweaning gain EPDs using the approximation method explained by Everett (1983). The correlations were generally low except for the Gulf Coast by Upper Plains correlation which was 1.00. The lowest correlation was .05 for the Lower Plains by Pacific region combinations. Table 27 presents the weighted average region estimates for postweaning gain from Table 26. Similar to birth weight, the Pacific region had the lowest (.22), and the Gulf Coast region had the highest (.48) estimated average correlations.

The weighted average correlation over all the regions for birth weight and postweaning gain from Table 27 were .24 and .32, respectively.

The correlations among sire EPDs across regions for birth weight and postweaning gain indicated that rank changes of EPDs were occurring for both traits; however, due to the small amounts of data available for these two traits, it is difficult to judge whether the correlations reflected true genetic performance differences of sires in different regions or simply reflect the inaccuracy of prediction within any one region. Future

Table 26. Average region estimates of birth weight and postweaning gain genetic correlations of sire expected progeny diferrences of sires with progeny in each of two regions of the United States

	Birth weight		Postweaning gain	
Region[a]	Correlation[b]	Total number of sires	Correlation[b]	Total number of sires
Northeast	.19	706	.38	829
Cornbelt	.25	764	.26	863
South	.27	741	.28	882
Gulf Coast	.34	350	.48	476
Upper Plains	.30	447	.36	685
Lower Plains	.28	694	.29	994
Rocky Mts.	.29	505	.43	617
Desert S.W.	.26	410	.25	545
Pacific[c]	.05	541	.22	639
Weighted average	.25	2579	.32	3265

[a]Each region correlation was calculated by weighting each region by region correlation by the number of sires, summing across the region by region correlations that contain the region of interest and dividing the sum by the total number of sires.

[b]The genetic correlation estimates use approximation procedures explained by Everett (1983).

[c]The weighted average was calculated by weighting each region by region correlation by the number of sires, summing across all region by region correlations and dividing the sum by the total number of sires.

Table 27. Estimates of postweaning genetic correlations of sire expected progeny differences of sires with progeny in each of two regions of the United States

Region:	Cornbelt	South	Gulf Coast	Upper Plains	Lower Plains	Rocky Mts.	Desert S.W.	Pacific
Northeast	.18[a] 145[b]	.22 125	.71 60	.65 113	.35 145	.52 83	.49 73	.21 85
Cornbelt		.10 137	.20 59	.07 121	.45 183	.77 65	.24 69	.16 84
South			.28 122	.56 83	.24 170	.58 79	.23 67	.19 99
Gulf Coast				1.00 41	.41 81	.61 37	.58 37	.58 39
Upper Plains					.15 138	.32 85	.15 48	.43 56
Lower Plains						.45 106	.06 78	.05 93
Rocky Mts.							.16 76	.21 86
Desert S.W.								.25 97

[a]The genetic correlation estimates for EPDs of sires with progeny in two different regions using approximation procedures explained by Everett (1983).

[b]The number of sires with progeny in the two regions.

analyses of birth weight and postweaning gain involving larger sets of data should improve the estimations of the true nature of region by sire, herd within region by sire and contemporary group within herd by sire interactions.

In general, the data indicated that performing sire evaluations across regions for birth weight, weaning weight and postweaning gain while assuming that region by sire effects are negligible may lead to severe errors in ranking sires for future progeny performance in some regions. It would appear that performing separate sire evaluation analyses for each region would provide more accurate information on sire future progeny performance within any one region.

SUMMARY

The importance of region by sire, herd within region by sire and contemporary group within herd by sire interactions were evaluated for 68,271 birth weight, 247,943 weaning weight and 98,790 postweaning gain records supplied by the American Polled Hereford Association. Variance components for sire, region by sire, herd within region by sire, contemporary group within herd by sire and error were estimated using Henderson Method 3 estimation procedures. Sire by region, herd within region by sire and contemporary group within herd by sire variance estimates divided by the sire variance estimate were .57, .93 and 1.71, respectively, for weaning weight, -1.00, -.14 and 1.29, respectively, for birth weight, and -1.19, .14 and 1.22, respectively, for postweaning gain.

The average genetic correlation estimates of weaning weight sire expected progeny differences (EPDs) across regions was .64. This value expresses the correlation among progeny of the same sire after the sire evaluation model had accounted for the contemporary group within herd by sire and herd within region by sire interactions. The average genetic correlation estimates of weaning weight sire EPDs across contemporary groups within herds and across herds within regions were .37 and .27, respectively. The correlation estimates indicated that some rank changes were occurring between sire EPDs in different regions, and substantial rank changes of sire EPDs were occurring across herds and contemporary group. Heritability

of weaning weight was .11 across region, .17 across herds within region .28 within herds, and .46 within contemporary group.

The average genetic correlation estimate among birth weight sire EPDs across regions was .24 and .35 using two different estimation methods. The average genetic correlation estimate among postweaning gain sire EPDs across regions was .21 and .32 using two different estimation methods. The correlation estimates for birth weight and postweaning gain may not fully reflect the true nature of the correlations due to insufficient number of progeny across regions.

In general, contemporary group within herd by sire interaction appeared to be an important source of variation for all the traits and should continue to be included as a random effect in future national sire evaluations for the Polled Hereford breed. The data also indicated that performing sire evaluations across regions for birth weight, weaning weight and postweaning gain, while assuming that region by sire effects are negligible, may lead to severe errors in ranking sires in some regions. Separate sire evaluations for each region would yield sire estimates that better reflect the true future progeny performance of a sire in each region.

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